


```
QY 121 DQFALYKEDGDPAPKNEBWRVRSFPIITVTAHSGTYRCYCSFSSRDPYLMASPSDPLEL 180
|
|
|
Db 121 DQFALYKEDGDPAPKNEBWRVRSFPIITVTAHSGTYRCYCSFSSRDPYLMASPSDPLEL 180
QY 181 VVTGTSVTPSRLLPTEPPSSVAEFSSEATAEELTVSFNNKVFTEITSRSITTSPKESDSPAG 240
|
|
|
Db 181 VVTGTSVTPSRLLPTEPPSSVAEFSSEATAEELTVSFNNKVFTEITSRSITTSPKESDSPAG 240
QY 241 ARQYTTKGN 249
|
|
|
Db 241 ARQYTTKGN 249

RESULT 2
US-09-832-312-5
; Sequence 5, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-832-312-5

Query Match 100.0%; Score 1304; DB 9; Length 319;
Best Local Similarity 100.0%; Pred. No. 6.6e-104;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQGPVVDLYRLKLSRRYQDQAVLFIPAMKR 60
|
|
|
Db 1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQGPVVDLYRLKLSRRYQDQAVLFIPAMKR 60
QY 61 SLAGRYRCSYQNGSLMSPDQLELVATGVFAKPSLSAQDPAVSSGGDVTLLCCQTRYGF 120
|
|
|
Db 61 SLAGRYRCSYQNGSLMSPDQLELVATGVFAKPSLSAQDPAVSSGGDVTLLCCQTRYGF 120
QY 121 DQFALYKEDGDPAPKNEBWRVRSFPIITVTAHSGTYRCYCSFSSRDPYLMASPSDPLEL 180
|
|
|
Db 121 DQFALYKEDGDPAPKNEBWRVRSFPIITVTAHSGTYRCYCSFSSRDPYLMASPSDPLEL 180
QY 181 VVTGTSVTPSRLLPTEPPSSVAEFSSEATAEELTVSFNNKVFTEITSRSITTSPKESDSPAG 240
|
|
|
Db 181 VVTGTSVTPSRLLPTEPPSSVAEFSSEATAEELTVSFNNKVFTEITSRSITTSPKESDSPAG 240
QY 241 ARQYTTKGN 249
|
|
|
Db 241 ARQYTTKGN 249

RESULT 3
US-09-832-312-3
; Sequence 3, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
```

```
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-832-312-3

Query Match 100.0%; Score 1304; DB 9; Length 339;
Best Local Similarity 100.0%; Pred. No. 7.2e-104;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQGPVVDLYRLKLSRRYQDQAVLFIPAMKR 60
|
|
|
Db 1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQGPVVDLYRLKLSRRYQDQAVLFIPAMKR 60
QY 61 SLAGRYRCSYQNGSLMSPDQLELVATGVFAKPSLSAQDPAVSSGGDVTLLCCQTRYGF 120
|
|
|
Db 61 SLAGRYRCSYQNGSLMSPDQLELVATGVFAKPSLSAQDPAVSSGGDVTLLCCQTRYGF 120
QY 121 DQFALYKEDGDPAPKNEBWRVRSFPIITVTAHSGTYRCYCSFSSRDPYLMASPSDPLEL 180
|
|
|
Db 121 DQFALYKEDGDPAPKNEBWRVRSFPIITVTAHSGTYRCYCSFSSRDPYLMASPSDPLEL 180
QY 181 VVTGTSVTPSRLLPTEPPSSVAEFSSEATAEELTVSFNNKVFTEITSRSITTSPKESDSPAG 240
|
|
|
Db 181 VVTGTSVTPSRLLPTEPPSSVAEFSSEATAEELTVSFNNKVFTEITSRSITTSPKESDSPAG 240
QY 241 ARQYTTKGN 249
|
|
|
Db 241 ARQYTTKGN 249

RESULT 4
US-10-157-031-387
; Sequence 387, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashov, A. V.
; APPLICANT: Krutovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequen
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 387
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-157-031-387

Query Match 100.0%; Score 1304; DB 15; Length 339;
Best Local Similarity 100.0%; Pred. No. 7.2e-104;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQGPVVDLYRLKLSRRYQDQAVLFIPAMKR 60
|
|
|
Db 1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQGPVVDLYRLKLSRRYQDQAVLFIPAMKR 60
QY 21 QSGPLPKPSLQALPSSLVPLEKPYTLRCQGPVVDLYRLKLSRRYQDQAVLFIPAMKR 80
|
|
|
Db 21 QSGPLPKPSLQALPSSLVPLEKPYTLRCQGPVVDLYRLKLSRRYQDQAVLFIPAMKR 80
QY 61 SLAGRYRCSYQNGSLMSPDQLELVATGVFAKPSLSAQDPAVSSGGDVTLLCCQTRYGF 120
|
|
|
Db 61 SLAGRYRCSYQNGSLMSPDQLELVATGVFAKPSLSAQDPAVSSGGDVTLLCCQTRYGF 120
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Db      81 SLAGRYCSYQNGSLWLSLPSDQLELVACVFAKPSLSAQPGAVSSGGDVTLLQCTRYGF 140
      121 DQFALYKESGDPAPYKNERWYRASFPITITVTAHSGTYRCYSFSSRDYPLMSAPSDPEL 180
      141 DQFALYKESGDPAPYKNERWYRASFPITITVTAHSGTYRCYSFSSRDYPLMSAPSDPEL 200
Qy      181 VVTGTSVTPSRPLPTEPPSSVAEFSEATAEITVSTFNKVFTTETSITTSPEKSDSPAGP 240
      201 VVTGTSVTPSRPLPTEPPSSVAEFSEATAEITVSTFNKVFTTETSITTSPEKSDSPAGP 260
Cy      241 AROYTYTKGN 249
      261 AROYTYTKGN 269
Db
```

```
RESULT 5
US-10-446-826-37
; Sequence 37, Application US/10446826
; Publication No. US20030186885A1
; GENERAL INFORMATION:
; APPLICANT: TANDON, NARENDRA N.
; APPLICANT: SUN, BING
; APPLICANT: NAKAMURA, TAKASHI
; APPLICANT: YAMAMOTO, NAOMASA
; TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI) DNA AND
; TITLE OF INVENTION: PROTEIN SEQUENCES, AND USES THEREOF
; FILE REFERENCE: 03459, 0026-0000
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: US/09/653,255B
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: PCT/US00/23975
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,197
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: 60/158,251
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 37
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-446-826-37
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```
Query Match      100.0%; Score 1304; DB 12; Length 369;
Best Local Similarity 100.0%; Pred. No. 8e-104;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 QSGPLPRLSLQALPSSLVLEKPYTLRCQPGPVGLYRLKLSRRYQDQAVLFIPMKR 60
      98 QSGPLPRLSLQALPSSLVLEKPYTLRCQPGPVGLYRLKLSRRYQDQAVLFIPMKR 157
      61 SLAGRYCSYQNGSLWLSLPSDQLELVACVFAKPSLSAQPGAVSSGGDVTLLQCTRYGF 120
      156 SLAGRYCSYQNGSLWLSLPSDQLELVACVFAKPSLSAQPGAVSSGGDVTLLQCTRYGF 217
      121 DQFALYKESGDPAPYKNERWYRASFPITITVTAHSGTYRCYSFSSRDYPLMSAPSDPEL 180
      219 DQFALYKESGDPAPYKNERWYRASFPITITVTAHSGTYRCYSFSSRDYPLMSAPSDPEL 277
      181 VVTGTSVTPSRPLPTEPPSSVAEFSEATAEITVSTFNKVFTTETSITTSPEKSDSPAGP 240
      276 VVTGTSVTPSRPLPTEPPSSVAEFSEATAEITVSTFNKVFTTETSITTSPEKSDSPAGP 337
      241 AROYTYTKGN 249
      338 AROYTYTKGN 346
Db
```

RESULT 6
US-09-832-312-34

```
; Sequence 34, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,367
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PasteSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-34
```

```
Query Match      99.7%; Score 1300; DB 9; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.6e-103;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 QSGPLPRLSLQALPSSLVLEKPYTLRCQPGPVGLYRLKLSRRYQDQAVLFIPMKR 60
      21 QSGPLPRLSLQALPSSLVLEKPYTLRCQPGPVGLYRLKLSRRYQDQAVLFIPMKR 80
      61 SLAGRYCSYQNGSLWLSLPSDQLELVACVFAKPSLSAQPGAVSSGGDVTLLQCTRYGF 120
      81 SLAGRYCSYQNGSLWLSLPSDQLELVACVFAKPSLSAQPGAVSSGGDVTLLQCTRYGF 140
      121 DQFALYKESGDPAPYKNERWYRASFPITITVTAHSGTYRCYSFSSRDYPLMSAPSDPEL 180
      141 DQFALYKESGDPAPYKNERWYRASFPITITVTAHSGTYRCYSFSSRDYPLMSAPSDPEL 200
      181 VVTGTSVTPSRPLPTEPPSSVAEFSEATAEITVSTFNKVFTTETSITTSPEKSDSPAGP 240
      201 VVTGTSVTPSRPLPTEPPSSVAEFSEATAEITVSTFNKVFTTETSITTSPEKSDSPAGP 260
      241 AROYTYTKGN 249
      261 AROYTYTKGN 269
Db
```

```
RESULT 7
US-09-832-312-36
; Sequence 36, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,367
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PasteSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-09-832-312-36

Query Match 99.7%; Score 1300; DB 9; Length 339;
 Best Local Similarity 99.6%; Pred. No. 1.6e-103;
 Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVVDLYRLEKSSSRVQDQAVLFIAMKR 60
 DB 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVVDLYRLEKSSSRVQDQAVLFIAMKR 80
 QY 61 SLAGRYRCSYQNSLMSLPSDQLELVATGVFAKPSLSAOPGPAVSSGGVTLQCCOTRYGF 120
 DB 81 SLAGRYRCSYQNSLMSLPSDQLELVATGVFAKPSLSAOPGPAVSSGGVTLQCCOTRYGF 140
 QY 121 DQFALYKGGDPAPYKPERMYRASFPITVTAAHSGTYRCYSSSRDPYLMASDPLEL 180
 DB 141 DQFALYKGGDPAPYKPERMYRASFPITVTAAHSGTYRCYSSSRDPYLMASDPLEL 200
 QY 181 VVTGTSVTPSRPLTEPPSSVAEFSEATAEITVSTFNKVFTTETSRITTSFKESDSPAGP 240
 DB 201 VVTGTSVTPSRPLTEPPSSVAEFSEATAEITVSTFNKVFTTETSRITTSFKESDSPAGP 260
 QY 241 AROYTTKGN 249
 DB 261 AROYTTKGN 265

RESULT 8
 US-09-832-312-38
 ; Sequence 38; Application US/09632312
 ; Patent No. US20010049829A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Busfield et al.
 ; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
 ; FILE REFERENCE: 7853-234
 ; CURRENT APPLICATION NUMBER: US/09/832.312
 ; CURRENT FILING DATE: 2001-04-09
 ; PRIOR APPLICATION NUMBER: 09/610.118
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: 09/503.387
 ; PRIOR FILING DATE: 2000-02-14
 ; PRIOR APPLICATION NUMBER: 09/454.824
 ; PRIOR FILING DATE: 1999-12-06
 ; PRIOR APPLICATION NUMBER: 09/345.468
 ; PRIOR FILING DATE: 1999-06-30
 ; NUMBER OF SEQ ID NOS: 78
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 38
 ; LENGTH: 339
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-832-312-38

Query Match 99.7%; Score 1300; DB 9; Length 339;
 Best Local Similarity 99.6%; Pred. No. 1.6e-103;
 Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVVDLYRLEKSSSRVQDQAVLFIAMKR 60
 DB 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVVDLYRLEKSSSRVQDQAVLFIAMKR 80
 QY 61 SLAGRYRCSYQNSLMSLPSDQLELVATGVFAKPSLSAOPGPAVSSGGVTLQCCOTRYGF 120
 DB 81 SLAGRYRCSYQNSLMSLPSDQLELVATGVFAKPSLSAOPGPAVSSGGVTLQCCOTRYGF 140
 QY 121 DQFALYKGGDPAPYKPERMYRASFPITVTAAHSGTYRCYSSSRDPYLMASDPLEL 180
 DB 141 DQFALYKGGDPAPYKPERMYRASFPITVTAAHSGTYRCYSSSRDPYLMASDPLEL 200
 QY 181 VVTGTSVTPSRPLTEPPSSVAEFSEATAEITVSTFNKVFTTETSRITTSFKESDSPAGP 240
 DB 201 VVTGTSVTPSRPLTEPPSSVAEFSEATAEITVSTFNKVFTTETSRITTSFKESDSPAGP 260

QY 241 AROYTTKGN 249
 DB 261 AROYTTKGN 265

RESULT 9
 US-09-832-312-40
 ; Sequence 40; Application US/09832312
 ; Patent No. US20010049829A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Busfield et al.
 ; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
 ; FILE REFERENCE: 7853-234
 ; CURRENT APPLICATION NUMBER: US/09/832.312
 ; CURRENT FILING DATE: 2001-04-09
 ; PRIOR APPLICATION NUMBER: 09/610.118
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: 09/503.387
 ; PRIOR FILING DATE: 2000-02-14
 ; PRIOR APPLICATION NUMBER: 09/454.824
 ; PRIOR FILING DATE: 1999-12-06
 ; PRIOR APPLICATION NUMBER: 09/345.468
 ; PRIOR FILING DATE: 1999-06-30
 ; NUMBER OF SEQ ID NOS: 78
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 40
 ; LENGTH: 339
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-832-312-40

Query Match 99.7%; Score 1300; DB 9; Length 339;
 Best Local Similarity 99.6%; Pred. No. 1.6e-103;
 Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVVDLYRLEKSSSRVQDQAVLFIAMKR 60
 DB 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVVDLYRLEKSSSRVQDQAVLFIAMKR 80
 QY 61 SLAGRYRCSYQNSLMSLPSDQLELVATGVFAKPSLSAOPGPAVSSGGVTLQCCOTRYGF 120
 DB 81 SLAGRYRCSYQNSLMSLPSDQLELVATGVFAKPSLSAOPGPAVSSGGVTLQCCOTRYGF 140
 QY 121 DQFALYKGGDPAPYKPERMYRASFPITVTAAHSGTYRCYSSSRDPYLMASDPLEL 180
 DB 141 DQFALYKGGDPAPYKPERMYRASFPITVTAAHSGTYRCYSSSRDPYLMASDPLEL 200
 QY 181 VVTGTSVTPSRPLTEPPSSVAEFSEATAEITVSTFNKVFTTETSRITTSFKESDSPAGP 240
 DB 201 VVTGTSVTPSRPLTEPPSSVAEFSEATAEITVSTFNKVFTTETSRITTSFKESDSPAGP 260
 QY 241 AROYTTKGN 249
 DB 261 AROYTTKGN 265

RESULT 10
 US-10-446-826-5
 ; Sequence 5; Application US/10446826
 ; Publication No. US20030186885A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TANDON, NARENDRA N.
 ; APPLICANT: SUN, BING
 ; APPLICANT: NAKAMURA, TAKASHI
 ; APPLICANT: YAMAMOTO, NAOMASA
 ; TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI) DNA AND
 ; FILE REFERENCE: 03459.0026-00000
 ; CURRENT APPLICATION NUMBER: US/10/446.826
 ; CURRENT FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: US/09/653.255B
 ; PRIOR FILING DATE: 2000-08-31
 ; PRIOR APPLICATION NUMBER: PCT/US00/23975

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/ PRIOR FILING DATE: 2000-09-01
/ PRIOR APPLICATION NUMBER: 60/152,197
/ PRIOR FILING DATE: 1999-03-01
/ PRIOR APPLICATION NUMBER: 60/158,251
/ PRIOR FILING DATE: 1999-10-08
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: Patent Ver. 2.1
/ SEQ ID NO: 5
/ LENGTH: 339
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-0-446-826-5
```

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Query Match      97.9%; Score 1277; DB 12; Length 339;
Best Local Similarity 98.8%; Pred. No. 1,56-101;
Matches 246; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
CY 1  QSGPLPKPSLQALPSSLVPLEKPYTLRCQSPFGVDLYRLKLSRRYQDQAVLFIPIAKR 60
DB 21  QSGPLPKPSLQALPSSLVPLEKPYTLRCQSPFGVDLYRLKLSRRYQDQAVLFIPIAKR 80
CY 61  SLAGRYRCYQNGSLMSLPSCDQLELVATGVFAKPSLSAQGPVAVSSGGDVTLLCQCTRYGF 120
DB 81  SLAGRYRCYQNGSLMSLPSCDQLELVATGVFAKPSLSAQGPVAVSSGGDVTLLCQCTRYGF 140
CY 121  DQFALYKGGDPAPYKPEKMYRASFPITVTAAHSGTYRCYSSSRDPLYMSAPSDPLEL 180
DB 141  DQFALYKGGDPAPYKPEKMYRASFPITVTAAHSGTYRCYSSSRDPLYMSAPSDPLEL 200
CY 181  VVTGTSVTPSRPLPTEPPSSVAEFSEATAELTVSFINKVFTTETSRSITTSKESDSPA 240
DB 201  VVTGTSVTPSRPLPTEPPSSVAEFSEATAELTVSFINKVFTTETSRSITTSKESDSPA 260
CY 241  AROYTYKGN 249
DB 261  AROYTYKGN 269
```

RESULT 11

```
US-09-832-312-19
/ Sequence 19, Application US/09832312
/ Patent No. US20010049829A1
/ GENERAL INFORMATION:
/ APPLICANT: Buefield et al.
/ TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
/ FILE REFERENCE: 7853-234
/ CURRENT APPLICATION NUMBER: US/09/832,312
/ PRIOR FILING DATE: 2001-04-09
/ PRIOR APPLICATION NUMBER: 09/610,118
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: 09/503,387
/ PRIOR FILING DATE: 2000-02-14
/ PRIOR APPLICATION NUMBER: 09/454,824
/ PRIOR FILING DATE: 1999-12-06
/ PRIOR APPLICATION NUMBER: 09/345,468
/ PRIOR FILING DATE: 1998-06-30
/ NUMBER OF SEQ ID NOS: 78
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO: 19
/ LENGTH: 267
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-832-312-19
```

```
Query Match      68.7%; Score 895.5; DB 9; Length 267;
Best Local Similarity 69.9%; Pred. No. 66-69;
Matches 174; Conservative 18; Mismatches 54; Indels 3; Gaps 1;
```

```
CY 1  QSGPLPKPSLQALPSSLVPLEKPYTLRCQSPFGVDLYRLKLSRRYQDQAVLFIPIAKR 60
DB 22  QSGPLPKPSLQALPSSLVPLEKPYTLRCQSPFGVDLYRLKLSRRYQDQAVLFIPIAKR 81
CY 61  SLAGRYRCYQNGSLMSLPSCDQLELVATGVFAKPSLSAQGPVAVSSGGDVTLLCQCTRYGF 120
```

```
DB 82  SNAGRYRCYQNGSLMSLPSCDQLELVATGVFAKPSLSAQGPVAVSSGGDVTLLCQCTRYGF 141
CY 121  DQFALYKGGDPAPYKPEKMYRASFPITVTAAHSGTYRCYSSSRDPLYMSAPSDPLEL 180
DB 142  DQFALYKGGDPAPYKPEKMYRASFPITVTAAHSGTYRCYSSSRDPLYMSAPSDPLEL 201
CY 181  VVTGTSVTPSRPLPTEPPSSVAEFSEATAELTVSFINKVFTTETSRSITTSKESDSPA 240
DB 202  VVTGTSVTPSRPLPTEPPSSVAEFSEATAELTVSFINKVFTTETSRSITTSKESDSPA 258
CY 241  AROYTYKGN 249
DB 259  AROYTYKGN 267
```

RESULT 12

```
US-09-832-312-18
/ Sequence 18, Application US/09832312
/ Patent No. US20010049829A1
/ GENERAL INFORMATION:
/ APPLICANT: Buefield et al.
/ TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
/ FILE REFERENCE: 7853-234
/ CURRENT APPLICATION NUMBER: US/09/832,312
/ PRIOR FILING DATE: 2001-04-09
/ PRIOR APPLICATION NUMBER: 09/610,118
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: 09/503,387
/ PRIOR FILING DATE: 2000-02-14
/ PRIOR APPLICATION NUMBER: 09/454,824
/ PRIOR FILING DATE: 1999-12-06
/ PRIOR APPLICATION NUMBER: 09/345,468
/ PRIOR FILING DATE: 1998-06-30
/ NUMBER OF SEQ ID NOS: 78
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO: 18
/ LENGTH: 292
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-832-312-18
```

```
Query Match      68.7%; Score 895.5; DB 9; Length 292;
Best Local Similarity 69.9%; Pred. No. 67-69;
Matches 174; Conservative 18; Mismatches 54; Indels 3; Gaps 1;
```

```
CY 1  QSGPLPKPSLQALPSSLVPLEKPYTLRCQSPFGVDLYRLKLSRRYQDQAVLFIPIAKR 60
DB 1  QSGPLPKPSLQALPSSLVPLEKPYTLRCQSPFGVDLYRLKLSRRYQDQAVLFIPIAKR 60
CY 61  SLAGRYRCYQNGSLMSLPSCDQLELVATGVFAKPSLSAQGPVAVSSGGDVTLLCQCTRYGF 120
DB 61  SLAGRYRCYQNGSLMSLPSCDQLELVATGVFAKPSLSAQGPVAVSSGGDVTLLCQCTRYGF 120
CY 121  DQFALYKGGDPAPYKPEKMYRASFPITVTAAHSGTYRCYSSSRDPLYMSAPSDPLEL 180
DB 121  DQFALYKGGDPAPYKPEKMYRASFPITVTAAHSGTYRCYSSSRDPLYMSAPSDPLEL 180
CY 181  VVTGTSVTPSRPLPTEPPSSVAEFSEATAELTVSFINKVFTTETSRSITTSKESDSPA 240
DB 181  VVTGTSVTPSRPLPTEPPSSVAEFSEATAELTVSFINKVFTTETSRSITTSKESDSPA 240
CY 241  AROYTYKGN 249
DB 241  AROYTYKGN 249
```

RESULT 13

```
US-09-832-312-16
/ Sequence 16, Application US/09832312
/ Patent No. US20010049829A1
/ GENERAL INFORMATION:
/ APPLICANT: Buefield et al.
```

FILE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/832,312
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 16
LENGTH: 313
TYPE: PRT
ORGANISM: Mus musculus
US-09-832-312-16

Query Match 68.7%; Score 895.5; DB 9; Length 313;
Best Local Similarity 69.9%; Pred. No. 7,3e-69;
Matches 174; Conservative 18; Mismatches 54; Indels 3; Gaps 1;

QY 1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQSPGVLDYRLKLSRRYQDAVLFIPIAMKR 60
DB 22 QSGPLPKPSLQALPSSLVPLEKPYTLRCQSPGVLDYRLKLSRRYQDAVLFIPIAMKR 8;
QY 61 SLAGRYCSYONGSLMSLPDQLELVATGVFAKPSASQGPVAVSSGDDVTLCQCTRYGF 120
DB 82 SNAGRYCSYONGSHMSLPDQLELVATGVFAKPSASAHSSAVPGQRTVTLKQSPYSF 14;
QY 121 DQFALYKGGDPAKYKPERMYRASFTITVTAHSGTYRCYSFSSRDPLYMSAPSDPLEL 180
DB 142 DEFVLKSGDTGPKRPEKMYRANFPIITVTAHSGTYRCYSFSSRDPLYMSAPSDPLEL 20;
QY 181 VVTGTSVTPSRPLTEPSSVAEFSEATLTVSFTNKVFITTESSRITTSPEKSDSPAGP 240
DB 202 VVTGLSATPSQVPTPESSFPVTESSRRPSILP---TKISTTEKKNITASPEGLSPIGF 258
QY 241 ARQYTTKGN 249
DB 259 AHQHYAKGN 267

RESULT 14
US-09-832-312-48
Sequence 48; Application US/09832312
Patent No. US20010049829A1
GENERAL INFORMATION:
APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/832,312
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 48
LENGTH: 313
TYPE: PRT
ORGANISM: Mus musculus
US-09-832-312-48

Query Match 68.7%; Score 895.5; DB 9; Length 313;
Best Local Similarity 69.9%; Pred. No. 7,3e-69;

Matches 174; Conservative 18; Mismatches 54; Indels 3; Gaps 1;
QY 1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQSPGVLDYRLKLSRRYQDAVLFIPIAMKR 60
DB 22 QSGPLPKPSLQALPSSLVPLEKPYTLRCQSPGVLDYRLKLSRRYQDAVLFIPIAMKR 81
QY 61 SLAGRYCSYONGSLMSLPDQLELVATGVFAKPSASQGPVAVSSGDDVTLCQCTRYGF 120
DB 82 SNAGRYCSYONGSHMSLPDQLELVATGVFAKPSASAHSSAVPGQRTVTLKQSPYSF 141
QY 121 DQFALYKGGDPAKYKPERMYRASFTITVTAHSGTYRCYSFSSRDPLYMSAPSDPLEL 180
DB 142 DEFVLKSGDTGPKRPEKMYRANFPIITVTAHSGTYRCYSFSSRDPLYMSAPSDPLEL 20;
QY 181 VVTGTSVTPSRPLTEPSSVAEFSEATLTVSFTNKVFITTESSRITTSPEKSDSPAGP 240
DB 202 VVTGLSATPSQVPTPESSFPVTESSRRPSILP---TKISTTEKKNITASPEGLSPIGF 258
QY 241 ARQYTTKGN 249
DB 259 AHQHYAKGN 267

RESULT 15
US-09-832-312-42
Sequence 42; Application US/09832312
Patent No. US20010049829A1
GENERAL INFORMATION:
APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/832,312
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 42
LENGTH: 313
TYPE: PRT
ORGANISM: Mus musculus
US-09-832-312-42

Query Match 68.4%; Score 891.5; DB 9; Length 313;
Best Local Similarity 69.5%; Pred. No. 1.6e-68;
Matches 173; Conservative 18; Mismatches 55; Indels 3; Gaps 1;

QY 1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQSPGVLDYRLKLSRRYQDAVLFIPIAMKR 60
DB 22 QSGPLPKPSLQALPSSLVPLEKPYTLRCQSPGVLDYRLKLSRRYQDAVLFIPIAMKR 81
QY 61 SLAGRYCSYONGSLMSLPDQLELVATGVFAKPSASQGPVAVSSGDDVTLCQCTRYGF 120
DB 82 SNAGRYCSYONGSHMSLPDQLELVATGVFAKPSASAHSSAVPGQRTVTLKQSPYSF 141
QY 121 DQFALYKGGDPAKYKPERMYRASFTITVTAHSGTYRCYSFSSRDPLYMSAPSDPLEL 180
DB 142 DEFVLKSGDTGPKRPEKMYRANFPIITVTAHSGTYRCYSFSSRDPLYMSAPSDPLEL 201
QY 181 VVTGTSVTPSRPLTEPSSVAEFSEATLTVSFTNKVFITTESSRITTSPEKSDSPAGP 240
DB 202 VVTGLSATPSQVPTPESSFPVTESSRRPSILP---TKISTTEKKNITASPEGLSPIGF 258
QY 241 ARQYTTKGN 249
DB 259 AHQHYAKGN 267

Mon Nov 10 06:30:17 2003

us-09-503-387-9.rapb

Page 7

Search completed: November 10, 2003, 06:28:46
Job time : 446 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 10, 2003, 06:14:09 ; Search time 41 Seconds

(without alignments)
963,974 Million cell updates/sec

Title: US-09-503-387-9

Perfect score: 1364

Sequence: 1 QSGPLKPSJQALPSSIVPL.....SPKSDSPACPAFQYTKGN 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
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2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
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16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
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21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1364	100.0	249	22	Human TANGO 268 ex
2	1364	100.0	249	24	Human TANGO 268 ex
3	1364	100.0	319	22	Human TANGO 268 ex
4	1364	100.0	319	22	Human TANGO 268 ex
5	1364	100.0	319	22	Human TANGO 268 ex
6	1364	100.0	319	22	Human TANGO 268 ex
7	1364	100.0	319	22	Human TANGO 268 ex
8	1364	100.0	319	22	Human TANGO 268 ex
9	1364	100.0	501	24	Human TANGO 268 ex

10	1364	100.0	512	24	ABF72519	Glycoprotein VI-1m
11	1364	99.7	339	22	ABF61273	Human TANGO 268-re
12	1364	99.7	339	22	ABF61274	Human TANGO 268-re
13	1364	99.7	339	22	ABF61275	Human TANGO 268-re
14	1364	99.7	339	22	ABF61276	Human TANGO 268-re
15	1364	99.7	339	24	ABU11239	Glycoprotein VI as
16	1364	99.7	339	24	ABU11240	Glycoprotein VI as
17	1364	99.7	339	24	ABU11241	Glycoprotein VI as
18	1364	99.7	339	24	ABU11242	Glycoprotein VI as
19	1364	99.7	339	22	ABU11243	Amino acid sequenc
20	1295	99.3	339	22	ABU11244	Human platelet mem
21	1277	97.9	339	22	ABU11245	Human platelet gly
22	1277	97.9	339	22	ABU11246	Mouse TANGO 268 ex
23	895.5	68.7	257	24	ABU11247	Mouse TANGO 268 ex
24	895.5	68.7	257	24	ABU11248	Mouse TANGO 268 ex
25	895.5	68.7	257	24	ABU11249	Mouse TANGO 268 ex
26	895.5	68.7	257	24	ABU11250	Mouse TANGO 268 ex
27	895.5	68.7	257	24	ABU11251	Mouse TANGO 268 ex
28	895.5	68.7	257	24	ABU11252	Mouse TANGO 268 ex
29	895.5	68.7	257	24	ABU11253	Mouse TANGO 268 ex
30	891.5	68.4	333	22	ABF61277	Mouse TANGO 268-re
31	891.5	68.4	333	22	ABF61278	Mouse TANGO 268-re
32	891.5	68.4	333	22	ABF61279	Mouse TANGO 268-re
33	891.5	68.4	333	22	ABU11243	Glycoprotein VI as
34	891.5	68.4	333	24	ABU11244	Glycoprotein VI as
35	891.5	68.4	333	24	ABU11245	Glycoprotein VI as
36	418	32.1	448	19	AAH82551	Human LIR-Pbm2 pro
37	418	32.1	448	19	AAH82552	Human gp49.Hm.8 po
38	418	32.1	448	21	AAH82553	Human gp49.Hm.8 po
39	418	32.1	448	21	AAH82554	Human gp49.Hm.8 po
40	418	32.1	448	21	AAH82555	Human gp49.Hm.8 po
41	408.5	31.3	632	24	ABU11268	Human TANGO 268 ex
42	408.5	31.3	632	24	ABU11269	Human TANGO 268 ex
43	408.5	31.3	632	24	ABU11270	Human TANGO 268 ex
44	408.5	31.3	632	24	ABU11271	Human TANGO 268 ex
45	404.5	31.0	500	22	ABF10579	Human macrophage-e

ALIGNMENTS

AA61261	1	AA61261 standard; Protein; 249 AA.
AC	AA61261	
XX	04-APR-2001	(first entry)
DE	Human TANGO 268 extracellular domain.	
XX	Human; TANGO 268; cardiac; cerebroprotective; cytosolic; antithrombotic; antiproteolytic; haemostatic; glycoprotein VI; GPIIb/IIIa; platelet membrane glycoprotein receptor; bleeding disorder; blood vessel injury; thrombotic disorder; haemorrhagic disorder; ischaemia; cardiovascular disease; immunological disease; liver disorder; cancer.	
OS	Homo sapiens.	
XX	WO200100810-A1.	
XX	04-JAN-2001.	
XX	30-JUN-2000; 2000KW-US18152.	
XX	30-JUN-1999; 99US-0345468.	
XX	06-DEC-1999; 99US-0454824.	
XX	14-FEB-2000; 2000US-0503387.	
XX	(MIL-) NILENNIUM PHARM INC.	
XX	Busfield SJ, Valleria J, Jardot-Perrus M, Vainchenker W, Gill DS;	

PI Qian WD, Kingsbury G;
XX
XX WPI; 2001-030877/03.
XX
XX New genes encoding human platelet-expressed collagen receptor.
PT glycoprotein VI, and its modulators, useful for preventing, treating
PT and diagnosing hemorrhagic disorders, thrombotic diseases and
PT immunological disorders.
XX
XX Disclosure; Page 203-204; 227pp; English.
XX
XX The present sequence is given in a specification relating to an isolated
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC glycoprotein VI (GPVI), also called TAMGO 268. The GPVI polynucleotides
CC and polypeptides and their modulators, e.g. antisense nucleic acids,
CC ribozymes and antibodies, are useful for preventing, treating and
CC diagnosing disorders associated with aberrant expression or activity of
CC GPVI. These disorders include bleeding disorders
CC (e.g. thrombocytopenia), blood vessel injury, thrombotic disorders
CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
CC infarction), immunological diseases (e.g. platelet disorder) and
CC erythronic liver disorders. Preferably they are used to prevent acute
CC cardiac ischaemia following angioplasty and metastatic cancers,
CC especially of the colon and liver.
XX
XX Sequence 249 AA;
SQ
Query Match: 100.0%; Score 1304; DB 24; Length 249;
Best Local Similarity 100.0%; Pred No. 2.3e-105;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QSGPLPKPSQALPSSVPLEKPVTLRCQSPGVLDYLRLEKSSSRVQDAVLFIPAMKR 60
Db 1 QSGPLPKPSQALPSSVPLEKPVTLRCQSPGVLDYLRLEKSSSRVQDAVLFIPAMKR 60
QY 61 SLAGRYRCSYQNGSLMSLPSDQLELVATGVFAKPSLSAQGPAVSSGCVTLQCCQRYGF 120
Db 61 SLAGRYRCSYQNGSLMSLPSDQLELVATGVFAKPSLSAQGPAVSSGCVTLQCCQRYGF 120
QY 121 DQFALYKGGPAPAKNERKWRASFPITVTAAHSGTYRCPSSSRQPYLWSAFSPDTEL 180
Db 121 DQFALYKGGPAPAKNERKWRASFPITVTAAHSGTYRCPSSSRQPYLWSAFSPDTEL 180
QY 181 VYTGTSVTPSRRLPTEPPSSVAEFSDEATLTVSFTNKVFTTSRSLTSPKSSSPAGP 240
Db 181 VYTGTSVTPSRRLPTEPPSSVAEFSDEATLTVSFTNKVFTTSRSLTSPKSSSPAGP 240
QY 241 AFOYTTKGN 249
Db 241 AFOYTTKGN 249
DB
RESULT 2
ABU11227
ID ABU11227 standard; Peptide: 249 AA.
XX
XX ABU11227;
AC
XX
XX 06-FEB-2003 (first entry)
DT
XX
XX Human TAMGO 268 extracellular domain.
DE
XX
XX Human; mouse; variable heavy; VH; antigen: cancer;
XX complementarity determining region; TAMGO 268, glycoprotein VI; GPVI;
XX TAMGO 268; extracellular matrix; collagen; platelet release;
XX proinfection; migration; embryogenesis; inflammation; thrombosis;
XX degeneration; thrombocytopenia; antibody; thrombotic disorder;
XX cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
XX leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
XX cardiovascular disease; angina pectoris; myocardial infarction;
XX coronary restenosis; atherosclerosis; immunological disorder;

XX developmental disorder; embryonic disorder; liver disorder;
XX cerebral vascular disease; venous thromboembolism disease.
XX
XX Homo sapiens.
OS
XX
XX K0200280368-A1.
PK
XX
XX 17-OCT-2002.
PD
XX
XX 03-APR-2002; 2002MO-US:1122.
PF
XX
XX 03-APR-2001; 2001US-0829495.
PR
XX
XX (MILL) XILLENIUM PHARM INC.
PA
XX
XX Busfield SJ, Villavea J, Jandroz-Perrus W, Vanhencken W, Gill ES,
PI Qian WM, Kingsbury G;
PI WPI; 2003-058477/05.
XX
XX
XX Disclosure; Page 212-213; 236pp; English.
XX
XX This invention relates to a novel purified antibody comprising a
CC variable heavy (VH) complementarity determining region (CDR1, VH CDR2
CC or VH CDR3, or variable light (VL) CDR1, VL CDR2 or VL CDR3, and
CC immunospecifically binding to a TAMGO 268 (also referred as glycoprotein
CC VI (GPVI)) antigen. The antibodies of the invention act to decrease or
CC block TAMGO 268 binding to extracellular matrix components, or as a
CC collagen or platelet release and aggregation blocker. The antibodies of
CC the invention are useful for modulating proliferation, migration,
CC morphology, differentiation and/or function of megakaryocytes and
CC platelets, including during development e.g. embryogenesis; modulating
CC leukocyte-platelet and platelet-endothelium interactions in
CC inflammation and/or thrombosis, and modulating platelet aggregation and
CC degranulation. They are also useful for modulating disorders associated
CC with abnormal or aberrant megakaryocyte and/or platelet proliferation,
CC migration, morphology, differentiation and/or function, e.g. bleeding
CC disorders such as thrombocytopenia. Other diseases which may be
CC modulated by these antibodies are thrombotic disorders, cerebral
CC vascular diseases (e.g. stroke and ischaemia) venous thromboembolism
CC diseases (e.g. diseases involving leg swelling, pain and ulceration,
CC pulmonary embolism, etc); coronary diseases (e.g. cardiovascular
CC diseases including angina pectoris, myocardial infarction, coronary
CC restenosis, atherosclerosis, etc); immunological disorders,
CC developmental disorders, erythronic disorders, liver disorders, cerebral
CC vascular diseases, venous thromboembolism disease, coronary diseases,
CC and metastatic cancers. The antibodies of the invention only causes a
CC transient decrease in platelet counts, platelet aggregation, and/or
CC platelet activation and so have some advantages over prior art
CC methods. The present sequence represents a peptide sequence used to
CC generate the antibodies of the invention.
XX
XX Sequence 249 AA;
SQ
Query Match: 100.0%; Score 1304; DB 24; Length 249;
Best Local Similarity 100.0%; Pred No. 2.3e-105;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QSGPLPKPSQALPSSVPLEKPVTLRCQSPGVLDYLRLEKSSSRVQDAVLFIPAMKR 60
Db 1 QSGPLPKPSQALPSSVPLEKPVTLRCQSPGVLDYLRLEKSSSRVQDAVLFIPAMKR 60
QY 61 SLAGRYRCSYQNGSLMSLPSDQLELVATGVFAKPSLSAQGPAVSSGCVTLQCCQRYGF 120
Db 61 SLAGRYRCSYQNGSLMSLPSDQLELVATGVFAKPSLSAQGPAVSSGCVTLQCCQRYGF 120
QY 121 DQFALYKGGPAPAKNERKWRASFPITVTAAHSGTYRCPSSSRQPYLWSAFSPDTEL 180
Db 121 DQFALYKGGPAPAKNERKWRASFPITVTAAHSGTYRCPSSSRQPYLWSAFSPDTEL 180

Db 121 DGFALYKESDPAPKPERMYRASFLITVTAHSGTYRCYSSNDPFLMSAPSDPLEL 180
QY 181 VVTGTSVTPSRLLPTEPPSSVAEFSEATAEIVTSFTNKVFTTETSRSITTSPESSDPAGP 240
Db 181 VVTGTSVTPSRLLPTEPPSSVAEFSEATAEIVTSFTNKVFTTETSRSITTSPESSDPAGP 240
QY 241 AROYTYTKGN 249
Db 241 AROYTYTKGN 249

RESULT 3

AAB61257

ID AAB61257 standard; Protein; 313 AA.

AC AAB61257;

DT 04-APR-2001 (first entry)

DE Mature human TANGO 268 protein.

KM Human; TANGO 268; cardiac; cerebroprotective; cytosolic; anticoagulant;
thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
platelet membrane glycoprotein receptor; bleeding disorder;
KM blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KM ischaemia; cardiovascular disease; immunological disease; liver disorder;
KM cancer.

XX Homo sapiens.

XX MO200100810-A1.

XX 04-JAN-2001.

PF 30-JUN-2000; 2000MO-US18152.

PR 30-JUN-1999; 99US-0145468.

PR 06-DEC-1999; 99US-0454824.

PR 14-FEB-2000; 2000US-0503357.

XX (MILL-) MILLENNITUM PHARM INC.

XX Busfield SJ, Vilella C, Jandrot-Petrus M, Vaichenker W, Gill DS;
PI Qian XD, Kingsbury G;

XX WPI; 2001-380877/09.

XX New genes encoding human platelet-expressed collagen receptor,
PT glycoprotein VI, and its modulators, useful for preventing, treating
PT and diagnosing hemorrhagic disorders, thrombotic diseases and
PT immunological disorders -

XX Disclousure; Fig 2; 227pp; English.

XX The present sequence is given in a specification relating to an isolated
XX nucleic acid molecule encoding a platelet membrane glycoprotein receptor
XX Glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
XX and polypeptides and their modulators, e.g. antisense nucleic acids,
XX ribozymes and antibodies, are useful for preventing, treating and
XX diagnosing disorders associated with aberrant expression or activity of
XX GPVI. These disorders include bleeding disorders
XX (e.g. thrombocytopenia), blood vessel injury, thrombotic disorders
XX (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
XX disorders, coronary artery and cerebral artery diseases (e.g. stroke and
XX ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
XX infarction), immunological diseases (e.g. platelet disorder) and
XX embryonic liver disorders. Preferably they are used to prevent acute
XX cardiac ischaemia following angioplasty and metastatic cancers,
XX especially of the colon and liver.

SQ Sequence 319 AA;

Query Match 100.0%; Score 1304; DB 22; Length 319;

Best Local Similarity 100.0%; Pred. No. 3, 2e-105;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPPRSIQALPSSIVPLEKPVTLRCQPPGVDLVRLKSSSRVQDAVFPAMKR 60
Db 1 QSGPLPPRSIQALPSSIVPLEKPVTLRCQPPGVDLVRLKSSSRVQDAVFPAMKR 60
QY 61 SLARRHCSYQNGSLMSLPSDQELVATGVFAKPSLSACGPAVSSGGVATLCCOTRYGF 120
Db 61 SLARRHCSYQNGSLMSLPSDQELVATGVFAKPSLSACGPAVSSGGVATLCCOTRYGF 120
QY 121 DGFALYKESDPAPKPERMYRASFLITVTAHSGTYRCYSSNDPFLMSAPSDPLEL 180
Db 121 DGFALYKESDPAPKPERMYRASFLITVTAHSGTYRCYSSNDPFLMSAPSDPLEL 180
QY 181 VVTGTSVTPSRLLPTEPPSSVAEFSEATAEIVTSFTNKVFTTETSRSITTSPESSDPAGP 240
Db 181 VVTGTSVTPSRLLPTEPPSSVAEFSEATAEIVTSFTNKVFTTETSRSITTSPESSDPAGP 240
QY 241 AROYTYTKGN 249
Db 241 AROYTYTKGN 249

RESULT 4

AAB43403

ID AAB43403 standard; Protein; 319 AA.

AC AAB43403;

DT 05-MAR-2001 (first entry)

DE Human glycoprotein VI mature protein.

KM Human; thrombolytic; cardiac; glycoprotein VI; GPVI;
platelet membrane glycoprotein; platelet activation;
KM platelet-collagen interaction; thrombotic disorder;
KM cardiovascular disorder.

XX Homo sapiens.

XX MO200068377-A1.

XX 16-NOV-2000.

PF 25-APR-2000; 2000MO-EP03683.

PR 07-MAY-1999; 99EP-0109094.

XX (MERE) MERCK PATENT GMBH.

XX Ciemerson KJ;

XX WPI; 2001-007394/01.

XX N-PSDB; AAC83980.

XX Recombinant human glycoprotein VI, useful for treating thrombotic,
PT cardiovascular diseases or platelet-collagen interactions -

XX Claim 5; Fig 1; 27pp; English.

XX The present sequence is human glycoprotein VI (GPVI) mature protein. GPVI
XX is a platelet membrane glycoprotein which forms a complex together with
XX the Fc gamma common subunit, which is critical for platelet activation in
XX response to collagen. GPVI is useful as a screening tool for detecting
XX specific inhibitors of platelet-collagen interactions, and as a marker
XX for platelet age and platelet exposure to thrombotic and cardiovascular
XX disorders. GPVI is also useful for the manufacture of medicaments in the
XX therapeutic field of thrombotic and cardiovascular events, and disorders
XX related to platelet-collagen interactions.

SQ Sequence 319 AA;

Query Match 100.0%; Score 1394; DB 24; Length 319;
 Best Local Similarity 100.0%; Pred. No. 3.2e-105;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLYPLEKPYTLRCQGPVVDLYRLKLSRRYCDQAVLFIAMKR 60
 DB 1 QSGPLPKPSLQALPSSLYPLEKPYTLRCQGPVVDLYRLKLSRRYCDQAVLFIAMKR 60
 QY 61 SLGGRYCSYQNGSLMSLPDQJELVATGVFAKPSLSAQGPVAVSSGGVTLCCQRYGF 120
 DB 61 SLGGRYCSYQNGSLMSLPDQJELVATGVFAKPSLSAQGPVAVSSGGVTLCCQRYGF 120
 QY 121 DGFALYKEDDPAPYKPERWYRASFPITITVAASGTRCYSSFSRSDPYLMSAPSDPEL 180
 DB 121 DGFALYKEDDPAPYKPERWYRASFPITITVAASGTRCYSSFSRSDPYLMSAPSDPEL 180
 QY 181 VVTGTSVTPSRPLPTEPPSSVAEFSEATAEITVSTFNKVFETTSRSITTSFKESDSPAPG 240
 DB 181 VVTGTSVTPSRPLPTEPPSSVAEFSEATAEITVSTFNKVFETTSRSITTSFKESDSPAPG 240
 QY 241 AROYTTKGN 249
 DB 241 AROYTTKGN 249

RESULT 5
 ABB11223
 ID ABB11223 standard; Protein: 319 AA.
 AC ABB11223;
 DT 06-FEB-2003 (first entry)
 XX Human TANGO 268 mature protein.

DE Human TANGO 268 mature protein.
 XX Human; mouse; variable heavy; VH; antigen; cancer;
 KM complementarily determining region; TANGO 268; glycoprotein VI; GPII;
 KM TANGO 268; extracellular matrix; collagen; platelet release;
 KM proliferation; migration; embryogenesis; inflammation; thrombosis;
 KM degranulation; thrombocytopaenia; antibody; thrombotic disorder;
 KM cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
 KM 199 swelling; pain; ulceration; pulmonary embolism; coronary disease;
 KM cardiovascular disease; angina pectoris; myocardial infarction;
 KM coronary restenosis; atherosclerosis; immunological disorder;
 KM developmental disorder; embryonic disorder; liver disorder;
 KM cerebral vascular disease; venous thromboembolism disease.

XX Homo sapiens.
 XX MC30280968-A1.
 XX 17-OCT-2002.
 XX 09-APR-2002; 2002KC-US1122.
 XX 09-APR-2001; 2001US-0829495.
 XX (MIL-) MILLENNIUM PHARM INC.
 XX Busfield SJ, Villereal J, Jandrot-Perrus M, Vainchencker W, Gill DS;
 XX Qian DM, Kingsbury G;
 XX WFT; 2003-058477/05.

XX Novel substantially purified antibody immunospecifically binding to
 XX TANGO 268 antigen, useful for treating bleeding disorders such as
 XX thrombocytopaenia, stroke, ischaemia, pulmonary embolism, atherosclerosis
 XX -
 XX Disclosure: Page 211-212; 236pp; English.
 XX This invention relates to a novel purified antibody comprising a
 XX variable heavy (VH) complementarily determining region (CDR1), VH CDR2

CC or VH CDR3; or variable light (VL) CDR1, VL CDR2 or VL CDR3, and
 CC immunospecifically binding to a TANGO 268 (also referred as glycoprotein
 CC VI (GPII)) antigen. The antibodies of the invention act to decrease or
 CC block TANGO 268 binding to extracellular matrix components, or as a
 CC collagen or platelet release and aggregation blocker. The antibodies of
 CC the invention are useful for modulating proliferation, migration,
 CC morphology, differentiation and/or function of megakaryocytes and
 CC platelets, including during development e.g. embryogenesis, modulating
 CC leucocyte-platelet and platelet-endothelium interactions in
 CC inflammation and/or thrombosis, and modulating platelet aggregation and
 CC degradation. They are also useful for modulating disorders associated
 CC with abnormal or aberrant megakaryocyte and/or platelet proliferation,
 CC migration, morphology, differentiation and/or function, e.g. bleeding
 CC disorders such as thrombocytopaenia. Other diseases which may be
 CC modulated by these antibodies are thrombotic disorders, cerebral
 CC vascular diseases (e.g. stroke and ischaemia) venous thromboembolism
 CC diseases (e.g. diseases involving leg swelling, pain and ulceration,
 CC pulmonary embolism, etc); coronary diseases (e.g. cardiovascular
 CC diseases including angina pectoris, myocardial infarction, coronary
 CC restenosis, atherosclerosis, etc); immunological disorders,
 CC developmental disorders, embryonic disorders, liver disorders, cerebral
 CC vascular diseases, venous thromboembolism disease, coronary diseases,
 CC and metastatic cancers. The antibodies of the invention only causes a
 CC transient decrease in platelet counts, platelet aggregation, and/or
 CC platelet activation and so have some advantages over prior art
 CC methods. The present sequence represents a protein sequence used to
 CC create the antibodies of the invention.

XX Sequence 319 AA;

Query Match 100.0%; Score 1394; DB 24; Length 319;
 Best Local Similarity 100.0%; Pred. No. 3.2e-105;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLYPLEKPYTLRCQGPVVDLYRLKLSRRYCDQAVLFIAMKR 60
 DB 1 QSGPLPKPSLQALPSSLYPLEKPYTLRCQGPVVDLYRLKLSRRYCDQAVLFIAMKR 60
 QY 61 SLGGRYCSYQNGSLMSLPDQJELVATGVFAKPSLSAQGPVAVSSGGVTLCCQRYGF 120
 DB 61 SLGGRYCSYQNGSLMSLPDQJELVATGVFAKPSLSAQGPVAVSSGGVTLCCQRYGF 120
 QY 121 DGFALYKEDDPAPYKPERWYRASFPITITVAASGTRCYSSFSRSDPYLMSAPSDPEL 180
 DB 121 DGFALYKEDDPAPYKPERWYRASFPITITVAASGTRCYSSFSRSDPYLMSAPSDPEL 180
 QY 181 VVTGTSVTPSRPLPTEPPSSVAEFSEATAEITVSTFNKVFETTSRSITTSFKESDSPAPG 240
 DB 181 VVTGTSVTPSRPLPTEPPSSVAEFSEATAEITVSTFNKVFETTSRSITTSFKESDSPAPG 240
 QY 241 AROYTTKGN 249
 DB 241 AROYTTKGN 249

RESULT 6
 AAB61255
 ID AAB61255 standard; Protein: 339 AA.
 AC AAB61255;
 DT 04-APR-2001 (first entry)
 XX Human TANGO 268 protein.
 XX Human; TANGO 268; cardiant; cerebroprotective; cytosolic; anticoagulant;
 XX thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPII;
 KM platelet membrane glycoprotein receptor; bleeding disorder;
 KM blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
 KM ischaemia; cardiovascular disease; immunological disease; liver disorder;
 KM cancer.
 XX Homo sapiens.
 OS

XX
PN WO200200810-A1.
XX
PD 04-JAN-2001.
XX
PF 30-JUN-2000; 2002WO-US18152.
XX
PR 30-JUN-1999; 99US-0454468.
FR 06-DEC-1999; 99US-0454624.
PR 14-FEB-2000; 2000US-0503387.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Busfield SJ, Vilelala C, Jandrot-Perrus M, Vanhacker W, Gill DS;
PI Qian DM, Kingsbury G;
XX
DR MPI; 2001-080877/09.
CR N-PSDB; AAF29470, AAF29471.
XX
PT New genes encoding human platelet-expressed collagen receptor,
PT glycoprotein VI, and its modulators, useful for preventing, treating
PT and diagnosing hemorrhagic disorders, thrombotic diseases and
PT immunological disorders -
XX
PS Claim 8; fig 1A; 227pp; English.
XX
CC The present sequence is given in a specification relating to an isolated
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
CC and polypeptides and their modulators, e.g. antisense nucleic acids,
CC ribozymes and antibodies, are useful for preventing, treating and
CC diagnosing disorders associated with aberrant expression or activity of
CC GPVI. These disorders include bleeding disorders
CC (e.g. thrombocytopenia), blood vessel injury, thrombotic disorders
CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
CC infarction), immunological diseases (e.g. platelet disorder) and
CC embryonic liver disorders. Preferably they are used to prevent acute
CC cardiac ischaemia following angioplasty and metastatic cancers,
CC especially of the colon and liver.
XX
SQ Sequence 339 AA;
Query Match 100.0%; Score 1304; DB 22; length 339;
Best Local Similarity 100.0%; Pred. No. 3.5e-105;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QSGPLPKPSLQALPSSLVPEKPVTRRCQPGVDLYRLEKSSSRVQDAVLFPMKR 60
Db 21 QSGPLPKPSLQALPSSLVPEKPVTRRCQPGVDLYRLEKSSSRVQDAVLFPMKR 60
QY 61 SLGRRVRCYSQNGSJMSPSDQELVATGVFAKPSLSAQGPAVSSGGVTLQCCTRYGF 120
Db 81 SLGRRVRCYSQNGSJMSPSDQELVATGVFAKPSLSAQGPAVSSGGVTLQCCTRYGF 140
QY 121 LQCALYKSGPPAPYKPERMYRASFPIITTAHSGTRYCYSSSDPIYKSPFLSE 180
Db 141 LQCALYKSGPPAPYKPERMYRASFPIITTAHSGTRYCYSSSDPIYKSPFLSE 200
QY 181 VMTGTYTPRLPTPESSVAEPSEATLTVSFTKVFTEERSRSTISPKSDSPAG 240
Db 201 VMTGTYTPRLPTPESSVAEPSEATLTVSFTKVFTEERSRSTISPKSDSPAG 260
QY 241 ARQYTKGN 249
Db 261 ARQYTKGN 269
RESULT 7
ABU11221
ID ABU11221 standard; Protein: 339 AA.

AC ABU11221;
XX
XX 06-FEB-2003 (first entry)
XX
XX Human TANGO 268 protein.
XX
XX Human; mouse; variable heavy; VH; antigen; cancer;
XX complementarily determining region; TANGO 268; glycoprotein VI; GPVI;
XX TANGO 268; extracellular matrix; collagen; platelet release;
XX proliferation; migration; embryogenesis; inflammation; thrombosis;
XX degeneration; thrombocytopenia; antibody; thrombotic disorder;
XX cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
XX leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
XX cardiovascular disease; angina pectoris; myocardial infarction;
XX coronary restenosis; atherosclerosis; immunological disorder;
XX developmental disorder; embryonic disorder; liver disorder;
XX cerebral vascular disease; venous thromboembolism disease.
OS Homo sapiens.
XX
XX WO200200968-A1.
XX
XX 17-OCT-2002.
XX
XX 09-APR-2002; 2002WO-US11122.
XX
XX 09-APR-2001; 2001US-0829495.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Busfield SJ, Vilelala C, Jandrot-Perrus M, Vanhacker W, Gill DS;
XX Qian DM, Kingsbury G;
XX
XX MPI; 2001-050477/05.
XX
XX P-PSDB; ABX17291, ABX17290.
XX
XX Novel substantially purified antibody immunospecifically binding to
XX TANGO 268 antigen, useful for treating bleeding disorders such as
XX thrombocytopenia, stroke, ischaemia, pulmonary embolism, atherosclerosis
XX
XX
XX Disclosure; Figure 1; 236pp; English.
XX
XX This invention relates to a novel purified antibody comprising a
XX variable heavy (VH) complementarily determining region (CDR1, VH CDR2
XX or VH CDR3; or variable light (VL) CDR1, VL CDR2 or VL CDR3, and
XX immunospecifically binding to a TANGO 268 (also referred as glycoprotein
XX VI (GPVI)) antigen. The antibodies of the invention act to decrease or
XX block TANGO 268 binding to extracellular matrix components, or as a
XX collagen or platelet release and aggregation blocker. The antibodies of
XX the invention are useful for modulating proliferation, migration,
XX morphology, differentiation and/or function of megakaryocytes and
XX platelets, including during development e.g. embryogenesis, modulating
XX leukocyte-platelet and platelet-endothelium interactions in
XX inflammation and/or thrombosis, and modulating platelet aggregation and
XX degranulation. They are also useful for modulating disorders associated
XX with abnormal or aberrant megakaryocyte and/or platelet proliferation,
XX migration, morphology, differentiation and/or function, e.g. bleeding
XX disorders such as thrombocytopenia. Other diseases which may be
XX modulated by these antibodies are thrombotic disorders, cerebral
XX vascular diseases (e.g. stroke and ischaemia) venous thromboembolism
XX diseases (e.g. diseases involving leg swelling, pain and ulceration,
XX pulmonary embolism, etc); coronary diseases (e.g. cardiovascular
XX diseases including angina pectoris, myocardial infarction, coronary
XX restenosis, atherosclerosis, etc); immunological disorders,
XX developmental disorders, embryonic disorders, liver disorders, cerebral
XX vascular diseases, venous thromboembolism disease, coronary diseases,
XX and metastatic cancers. The antibodies of the invention only causes a
XX transient decrease in platelet counts, platelet aggregation, and/or
XX platelet activation and so have some advantages over prior art
XX methods. The present sequence represents a protein sequence used to
XX create the antibodies of the invention.

SC Sequence 339 AA;

Query Match 100.0%; Score 1304; DB 24; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.9e-105;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVLDYRLKXSSRRYQDQAVLFIAMKR 60
 DB 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVLDYRLKXSSRRYQDQAVLFIAMKR 80
 QY 61 SLAGRYRCSYONGSLMSLPSDQLELVATGVFAKPSLSAQGPVAVSSGGDVTLQCQTRYGF 120
 DB 81 SLAGRYRCSYONGSLMSLPSDQLELVATGVFAKPSLSAQGPVAVSSGGDVTLQCQTRYGF 140
 QY 121 DQFALYKEDDPAPYKNEERWYRASPFITVTAAHSGTYRCYSSSRDPYLMASPSPLEL 180
 DB 141 DQFALYKEDDPAPYKNEERWYRASPFITVTAAHSGTYRCYSSSRDPYLMASPSPLEL 200
 QY 181 VVTGTSVTPSRLLPTEPPSSVAEFSEATLTVSFTNKVFTTETSRITTSPEKSDSPAGP 240
 DB 201 VVTGTSVTPSRLLPTEPPSSVAEFSEATLTVSFTNKVFTTETSRITTSPEKSDSPAGP 260
 QY 241 ARQYTTKGN 249
 DB 261 ARQYTTKGN 269

RESULT 8
 AAY72791 standard; Protein; 369 AA.

AC AAY72791;
 XX 31-MAY-2001 (first entry)
 DE Human GPVI external domain yeast alpha factor chimera.
 XX Human; platelet membrane glycoprotein VI; GPVI; thrombolytic; therapy;
 KW vascular disease; thrombosis; plasmaid pPICZGPVI; chimeric protein.
 XX Chimeric - Homo sapiens.
 OS Chimeric - Homo sapiens.
 XX Key Location/Qualifiers
 FT 98..346
 FT /label= Human GPVI external domain
 FT /note= "Corresponds to 21-269 residues of human
 FT GPVI protein (AAY72791)."
 FT 347..363
 FT /label= Myc_epitope
 FT 364..369
 FT /label= His_tag
 XX Region
 XX MO200116321-A1.
 XX 08-MAR-2001.
 PD 01-SEP-2000; 2000MO-0S23975.
 XX 01-SEP-1999; 99US-0152197.
 PR 08-OCT-1999; 99US-0158251.
 XX (SUKA) OTSUKA PHARM CO LTD.
 PA Tandon N, Sun B, Nakamura T, Yamamoto N;
 PI WPI; 2001-226691/23.
 DR N-PSDB; AAD02863.
 XX Anti-thrombotic medicament, comprising a polypeptide having the
 PT extracellular domain of platelet membrane glycoprotein VI or its
 PT variant, useful for treating a vascular disease and reducing platelet
 PT activation -

XX Disclosure; Fig 5; 74pp; English.
 PS The present sequence is a chimeric protein encoded by pPICZGPVI
 CC DNA. The pPICZGPVI encodes human platelet membrane glycoprotein VI
 CC (GPVI) external domain, a yeast alpha-factor, tyc epitope and a
 CC histidine (His) tag. The pPICZGPVI is used to produce a soluble
 CC recombinant (sr) GPVI. The medicament comprising GPVI is useful for
 CC treating vascular disease, and for reducing platelet activation which
 CC involves contacting platelets with the medicament. The extracellular
 CC portion of GPVI is used therapeutically to attenuate platelet activation
 CC and aggregation and to treat thrombosis and other vascular diseases.
 CC Antibodies generated against GPVI are used as research and
 CC immunotherapeutic agents.

SO Sequence 369 AA;

Query Match 100.0%; Score 1304; DB 22; Length 369;
 Best Local Similarity 100.0%; Pred. No. 3.9e-105;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVLDYRLKXSSRRYQDQAVLFIAMKR 60
 DB 98 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVLDYRLKXSSRRYQDQAVLFIAMKR 157
 QY 61 SLAGRYRCSYONGSLMSLPSDQLELVATGVFAKPSLSAQGPVAVSSGGDVTLQCQTRYGF 120
 DB 158 SLAGRYRCSYONGSLMSLPSDQLELVATGVFAKPSLSAQGPVAVSSGGDVTLQCQTRYGF 217
 QY 121 DQFALYKEDDPAPYKNEERWYRASPFITVTAAHSGTYRCYSSSRDPYLMASPSPLEL 180
 DB 218 DQFALYKEDDPAPYKNEERWYRASPFITVTAAHSGTYRCYSSSRDPYLMASPSPLEL 277
 QY 181 VVTGTSVTPSRLLPTEPPSSVAEFSEATLTVSFTNKVFTTETSRITTSPEKSDSPAGP 240
 DB 278 VVTGTSVTPSRLLPTEPPSSVAEFSEATLTVSFTNKVFTTETSRITTSPEKSDSPAGP 337
 QY 241 ARQYTTKGN 249
 DB 338 ARQYTTKGN 346

RESULT 9
 ABP72518 standard; Protein; 501 AA.
 XX ABP72518;
 AC ABP72518;
 XX 23-MAY-2003 (first entry)
 DE Immunoglobulin Fc-glycoprotein VI fusion protein.
 XX Glycoprotein VI; GPVI; thrombolytic; anticoagulant; antiangiinal;
 KW cardiovascular; platelet; collagen; immunoglobulin; antibody;
 KW human; mouse; murine; drug screening; nonadhesive; surface coating.
 XX Chimeric - Homo sapiens.
 OS Chimeric - Mus sp.
 CS Synthetic.
 XX Key Location/Qualifiers
 FT 1..21
 FT /label= Mouse_antibody_signal_peptide
 FT 22..501
 FT /label= Mature_protein
 FT 22..249
 FT /label= Fc
 FT 250..252
 FT /label= Linker
 FT 253..501
 FT /label= Glycoprotein_VI
 XX Region
 XX MO2003008454-AA2.

XX 30-JAN-2003.
XX
XX 12-JUL-2002; 2002WO-EP07796.
XX
XX 18-JUL-2001; 2001EP-0116717.
XX
XX (MERCK) MERCK PATENT GMBH.
XX
XX Burger C, Gleitz J, Frech M;
XX WPI; 2003-229561/22.
XX
XX
XX New Glycoprotein VI (GPVI) fusion protein for preventing or treating
PT thrombotic or cardiovascular disorders, comprises a tag molecule and a
PT non-immunoglobulin molecule, e.g. protein or oligopeptide with
PT biological activity of GPVI -
PS
XX
XX Claim 9; Page 19-21; 42pp; English.
XX
XX The present sequence is that of a fusion protein comprising an
CC immunoglobulin Fc portion joined via a tripeptide linker to
CC glycoprotein VI (GPVI). The fusion protein includes a mouse antibody
CC N-terminal signal peptide. GPVI is a major platelet glycoprotein
CC which forms a complex with the Fc-gamma common subunit. The GPVI
CC subunit contains a collagen binding site and the Fc-gamma subunit is
CC responsible for signalling. The present Fc-GPVI fusion protein can
CC be obtained by recombinant DNA methods, and is an example of fusion
CC proteins of the invention in which GPVI is linked to a tag such as
CC myc, GST, HA, FLAG, STREP or, preferably, the Fc portion of an
CC immunoglobulin. Such fusion proteins can be used to screen for
CC agonists or antagonists of GPVI-collagen and/or platelet-collagen
CC interactions, and for the treatment of thrombotic and cardiovascular
CC events and disorders related to GPVI-collagen and/or platelet-collagen
CC interactions including increased platelet activation with collagen,
CC atherosclerotic plaque rupture, unstable angina or during surgical
CC treatment such as percutaneous transluminal coronary angioplasty
CC (claimed). The fusion proteins are also useful for coating
CC artificial surfaces to render them nonadhesive for cells, for
CC modifying intraocular lenses to lessen the thrombogenicity of the
CC lens material, for contacting the lens surface, and for covalent
CC crosslinking to modify the lens material (all claimed).
XX
XX
XX Sequence 501 AA;
SQ
Query Match 100.0%; Score 1304; DB 24; Length 501;
Best Local Similarity 100.0%; Pred. No. 5,9e-105;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 QSGPLPKPSLOALPSSIVLEKPYTLRQGGPGVDVRLKSSSYQDQAVLFPAKR 60
DB 253 QSGPLPKPSLOALPSSIVLEKPYTLRQGGPGVDVRLKSSSYQDQAVLFPAKR 312
XX
XX 61 SLGRVRCSTYONSLSLPSDQELVATGVFAKPSLACGPAVSSGGVDLTCCRYGF 120
DB 313 SLGRVRCSTYONSLSLPSDQELVATGVFAKPSLACGPAVSSGGVDLTCCRYGF 372
XX
XX 121 DQPALYKEGPPAPKPKNEKWRKASFPITITAAHSGVRCYSSSRDPYMSAPSPLE 180
DB 373 DQPALYKEGPPAPKPKNEKWRKASFPITITAAHSGVRCYSSSRDPYMSAPSPLE 432
XX
XX 181 VMTGTSVTPSRLPEPSSVAEFSEATAEVTFNTKVFTEERSGITTSPEKSSDPAG 240
DB 433 VMTGTSVTPSRLPEPSSVAEFSEATAEVTFNTKVFTEERSGITTSPEKSSDPAG 492
XX
XX 241 ARQYTTKGN 249
DB 493 ARQYTTKGN 501
XX
XX
XX RESULT 10
XX ABB72519 standard; Protein; 512 AA.
ID ABB72519

XX ABB72519;
XX
XX 23-MAY-2003 (first entry)
XX
XX Glycoprotein VI-immunoglobulin Fc fusion protein.
XX
XX Glycoprotein VI; GPVI; thrombolytic; anticoagulant; anti-anginal;
XX cardiovascular; platelet; collagen; immunoglobulin; antibody;
XX human; drug screening; nonadhesive; surface coating.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..25
XX FT /label= Oncostatin_M_signal_peptide
XX FT 26..512
XX FT /label= Mature_protein
XX FT 26..32
XX FT /label= Linker
XX FT 33..281
XX FT /label= Fc
XX FT 282..284
XX FT /label= Linker
XX FT 285..512
XX FT /label= Glycoprotein_VI
XX
XX WO2003008454-A2.
XX
XX 30-JAN-2003.
XX
XX 12-JUL-2002; 2002WO-EP07796.
XX
XX 18-JUL-2001; 2001EP-0116717.
XX
XX (MERCK) MERCK PATENT GMBH.
XX
XX Burger C, Gleitz J, Frech M;
XX WPI; 2003-229561/22.
XX
XX
XX New Glycoprotein VI (GPVI) fusion protein for preventing or treating
PT thrombotic or cardiovascular disorders, comprises a tag molecule and a
PT non-immunoglobulin molecule, e.g. protein or oligopeptide with
PT biological activity of GPVI -
PS
XX
XX Claim 9; Page 21-23; 42pp; English.
XX
XX The present sequence is that of a fusion protein comprising
CC glycoprotein VI (GPVI) joined via a tripeptide linker to the Fc
CC portion of immunoglobulin. The fusion protein includes a human
CC oncostatin M N-terminal signal peptide. GPVI is a major platelet
CC glycoprotein which forms a complex with the Fc-gamma common subunit.
CC The GPVI subunit contains a collagen binding site and the Fc-gamma
CC subunit is responsible for signalling. The present Fc-GPVI fusion
CC protein can be obtained by recombinant DNA methods, and is an example
CC of fusion proteins of the invention in which GPVI is linked to a tag
CC such as myc, GST, HA, FLAG, STREP or, preferably, the Fc portion of
CC an immunoglobulin. Such fusion proteins can be used to screen for
CC agonists or antagonists of GPVI-collagen and/or platelet-collagen
CC interactions, and for the treatment of thrombotic and cardiovascular
CC events and disorders related to GPVI-collagen and/or platelet-collagen
CC interactions including increased platelet activation with collagen,
CC atherosclerotic plaque rupture, unstable angina or during surgical
CC treatment such as percutaneous transluminal coronary angioplasty
CC (claimed). The fusion proteins are also useful for coating
CC artificial surfaces to render them nonadhesive for cells, for
CC modifying intraocular lenses to lessen the thrombogenicity of the
CC lens material, for contacting the lens surface, and for covalent
CC crosslinking to modify the lens material (all claimed).
XX
XX
XX Sequence 512 AA;
SQ

Query Match 100.0%; Score 1304; DB 24; Length 512;
Best Local Similarity 100.0%; Pred. No. 6e-105;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVLEKPYTLRCQGPVGVLYRLKLSRRYQDAVLFIPAMKR 60
DB 33 QSGPLPKPSLQALPSSLVLEKPYTLRCQGPVGVLYRLKLSRRYQDAVLFIPAMKR 92
QY 61 SLAGRYRCSYONGSLWSPSDQLELVATGVFAKPSLSAQGPVSSGGDVTLCQCRVGF 120
DB 93 SLAGRYRCSYONGSLWSPSDQLELVATGVFAKPSLSAQGPVSSGGDVTLCQCRVGF 152
QY 121 DQFALYKEDPAPYKNERWYRASFPITVTAHSGTYRCYFSRSSRDPYLSAPSDPLEL 180
DB 153 DQFALYKEDPAPYKNERWYRASFPITVTAHSGTYRCYFSRSSRDPYLSAPSDPLEL 212
QY 181 VWTGTSVTPSRLLPTEPPSSVAFSEATAEVTSFTNKVFTEESRSCTTSPEKSDSPAGP 240
DB 213 VWTGTSVTPSRLLPTEPPSSVAFSEATAEVTSFTNKVFTEESRSCTTSPEKSDSPAGP 272
QY 241 ARQYVTKGN 249
DB 273 ARQYVTKGN 281

RESULT 11
AAB61273
ID AAB61273 standard; Protein: 339 AA.
AC AAB61273;
XX
XX 04-APR-2001 (first entry)
DT
XX
DE Human TANGO 268-related protein #1.
XX
XX Human; TANGO 268; cardiact; cerebroprotective; cyostatic; anticoagulant;
KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW cancer.
XX
XX Homo sapiens.
OS
XX
XX W0200100810-A1.
PN
XX
XX 04-JAN-2001.
PD
XX
XX 30-JUN-2000; 2000MO-US-8152.
PF
XX
XX 30-JUN-1999; 99US-0345468.
PR 06-DEC-1999; 99US-0454824.
PR 14-FEB-2000; 2000US-0503387.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Busfield SJ, Villetal J, Jandrot-Perrus M, Vainchenker W, Gill DS;
PI Qian MD, Kingsbury G;
XX
XX WFI; 2001-080877/09.
DR N-PSDB; AAF29484.
XX
XX New genes encoding human platelet-expressed collagen receptor,
PT glycoprotein VI, and its modulators, useful for preventing, treating
PT and diagnosing hemorrbhic disorders, thrombotic diseases and
PT immunological disorders -
XX
XX Dielclosure; Page 213-214; 227pp; English.
XX
XX The present sequence is given in a specification relating to an isolated
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides

CC and polypeptides and their modulators, e.g. antisense nucleic acids,
CC ribozymes and antibodies, are useful for preventing, treating and
CC diagnosing disorders associated with aberrant expression or activity of
CC GPVI. These disorders include bleeding disorders
CC (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
CC infarction), immunological diseases (e.g. platelet disorder) and
CC embryonic liver disorders. preferably they are used to prevent acute
CC cardiac ischaemia following angioplasty and metastatic cancers,
CC especially of the colon and liver.
XX
XX
SQ Sequence 339 AA;
Query Match 99.7%; Score 1300; DB 22; Length 339;
Best Local Similarity 99.6%; Pred. No. 7.8e-105;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVLEKPYTLRCQGPVGVLYRLKLSRRYQDAVLFIPAMKR 60
DB 21 QSGPLPKPSLQALPSSLVLEKPYTLRCQGPVGVLYRLKLSRRYQDAVLFIPAMKR 80
QY 61 SLAGRYRCSYONGSLWSPSDQLELVATGVFAKPSLSAQGPVSSGGDVTLCQCRVGF 120
DB 81 SLAGRYRCSYONGSLWSPSDQLELVATGVFAKPSLSAQGPVSSGGDVTLCQCRVGF 140
QY 121 DQFALYKEDPAPYKNERWYRASFPITVTAHSGTYRCYFSRSSRDPYLSAPSDPLEL 180
DB 141 DQFALYKEDPAPYKNERWYRASFPITVTAHSGTYRCYFSRSSRDPYLSAPSDPLEL 200
QY 181 VWTGTSVTPSRLLPTEPPSSVAFSEATAEVTSFTNKVFTEESRSCTTSPEKSDSPAGP 240
DB 201 VWTGTSVTPSRLLPTEPPSSVAFSEATAEVTSFTNKVFTEESRSCTTSPEKSDSPAGP 260
QY 241 ARQYVTKGN 249
DB 261 ARQYVTKGN 269

RESULT 12
AAB61274
ID AAB61274 standard; Protein: 339 AA.
AC AAB61274;
XX
XX 04-APR-2001 (first entry)
DT
XX
DE Human TANGO 268-related protein #2.
XX
XX Human; TANGO 268; cardiact; cerebroprotective; cyostatic; anticoagulant;
KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW cancer.
XX
XX Homo sapiens.
OS
XX
XX W0200100810-A1.
PN
XX
XX 04-JAN-2001.
PD
XX
XX 30-JUN-2000; 2000MO-US-8152.
PF
XX
XX 30-JUN-1999; 99US-0345468.
PR 06-DEC-1999; 99US-0454824.
PR 14-FEB-2000; 2000US-0503387.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Busfield SJ, Villetal J, Jandrot-Perrus M, Vainchenker W, Gill DS;
PI Qian MD, Kingsbury G;

XX WPI: 2001-080877/09.
DR N-PSDB; AAF29485.
XX
XX New genes encoding human platelet-expressed collagen receptor,
PT glycoprotein VI, and its modulators, useful for preventing, treating
PT and diagnosing hemorrhagic disorders, thrombotic diseases and
PT immunological disorders -
XX
XX Disclosure: Page 214-215; 227pp; English.
XX
XX The present sequence is given in a specification relating to an isolated
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
CC and polypeptides and their modulators, e.g. antisense nucleic acids,
CC ribozymes and antibodies, are useful for preventing, treating and
CC diagnosing disorders associated with aberrant expression or activity of
CC GPVI. These disorders include bleeding disorders
CC (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
CC infarction), immunological diseases (e.g. platelet disorder) and
CC embryonic liver disorders. Preferably they are used to prevent acute
CC cardiac ischaemia following angioplasty and metastatic cancers,
CC especially of the colon and liver.
XX
XX Sequence 339 AA;
SQ
Query Match 99.7%; Score 1300; DB 22; Length 339;
Best Local Similarity 99.6%; Pred. No. 7.8e-105;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QSGPLPKPSIQALPSSIVPLEKPYTLRCQSPGVLDYRLKLSSSRYQDAVLFIPMKR 60
Db 21 QSGPLPKPSIQALPSSIVPLEKPYTLRCQSPGVLDYRLKLSSSRYQDAVLFIPMKR 80
QY 61 SLAGRYCSYONGSLWSPSDQLELVATGVFAKPSLAOPGPAVSSGCVTLCCOTRYGF 120
Db 61 SLAGRYCSYONGSLWSPSDQLELVATGVFAKPSLAOPGPAVSSGCVTLCCOTRYGF 140
QY 121 DOFALYKEDPAPYKNERMYRASFPITITVAHSGTYRCYSSSRDPYLSAPSDLEL 180
Db 141 DOFALYKEDPAPYKNERMYRASFPITITVAHSGTYRCYSSSRDPYLSAPSDLEL 200
QY 181 VVTGTSVTPSRPLTEPPSSVAEFSEATAEIVTSFTNKVFTTETSRITTSFKESDSPAGP 240
Db 201 VVTGTSVTPSRPLTEPPSSVAEFSEATAEIVTSFTNKVFTTETSRITTSFKESDSPAGP 260
QY 241 ARQYTTKGN 249
Db 261 ARQYTTKGN 269
RESULT 13
AA61275
ID AAB61275 standard; Protein: 339 AA.
XX
XX AAB61275;
XX
XX 04-APR-2001 (first entry)
XX
XX Human TANGO 268-related protein #3.
XX
XX Human; TANGO 268; cariant; cerebroprotective; cytostatic; anticoagulant;
KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
XX
XX
XX Homo sapiens.
XX

PN W0200100810-A1.
XX
XX 04-JAN-2001.
PD
XX
XX 30-JUN-2000; 2000MO-US18152.
PF
XX 30-JUN-1999; 99US-0345468.
PR 06-DEC-1999; 99US-0454624.
PR 14-FEB-2000; 2000US-0503387.
XX
XX (MIL-1) MILLENNIUM PHARM INC.
XX
XX Busfield SJ, Villalal J, Candrot-Perrus M, Vainchencker W, Gall DS;
PI Qian MD, Kingsbury G;
XX
XX WPI: 2001-080877/09.
DR N-PSDB; AAF29486.
XX
XX New genes encoding human platelet-expressed collagen receptor,
PT glycoprotein VI, and its modulators, useful for preventing, treating
PT and diagnosing hemorrhagic disorders, thrombotic diseases and
PT immunological disorders -
XX
XX Disclosure: Page 216; 227pp; English.
XX
XX The present sequence is given in a specification relating to an isolated
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
CC and polypeptides and their modulators, e.g. antisense nucleic acids,
CC ribozymes and antibodies, are useful for preventing, treating and
CC diagnosing disorders associated with aberrant expression or activity of
CC GPVI. These disorders include bleeding disorders
CC (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
CC infarction), immunological diseases (e.g. platelet disorder) and
CC embryonic liver disorders. Preferably they are used to prevent acute
CC cardiac ischaemia following angioplasty and metastatic cancers,
CC especially of the colon and liver.
XX
XX Sequence 339 AA;
SQ
Query Match 99.7%; Score 1300; DB 22; Length 339;
Best Local Similarity 99.6%; Pred. No. 7.8e-105;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QSGPLPKPSIQALPSSIVPLEKPYTLRCQSPGVLDYRLKLSSSRYQDAVLFIPMKR 60
Db 21 QSGPLPKPSIQALPSSIVPLEKPYTLRCQSPGVLDYRLKLSSSRYQDAVLFIPMKR 80
QY 61 SLAGRYCSYONGSLWSPSDQLELVATGVFAKPSLAOPGPAVSSGCVTLCCOTRYGF 120
Db 61 SLAGRYCSYONGSLWSPSDQLELVATGVFAKPSLAOPGPAVSSGCVTLCCOTRYGF 140
QY 121 DOFALYKEDPAPYKNERMYRASFPITITVAHSGTYRCYSSSRDPYLSAPSDLEL 180
Db 141 DOFALYKEDPAPYKNERMYRASFPITITVAHSGTYRCYSSSRDPYLSAPSDLEL 200
QY 181 VVTGTSVTPSRPLTEPPSSVAEFSEATAEIVTSFTNKVFTTETSRITTSFKESDSPAGP 240
Db 201 VVTGTSVTPSRPLTEPPSSVAEFSEATAEIVTSFTNKVFTTETSRITTSFKESDSPAGP 260
QY 241 ARQYTTKGN 249
Db 261 ARQYTTKGN 269
RESULT 14
AAB61276
ID AAB61276 standard; Protein: 339 AA.
XX
XX AAB61276;
AC

XX 04-APR-2001 (first entry)

XX Human TANGO 268-related protein #4.

XX Human; TANGO 268: cardiant; cerebroprotective; cytosolic; anticoagulant;
 XX thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
 XX platelet membrane glycoprotein receptor; bleeding disorder;
 XX blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
 XX ischaemia; cardiovascular disease; immunological disease; liver disorder;
 XX cancer.

XX Homo sapiens.

XX WO2001:00810-A1.

XX C4-JAN-2001.

XX 30-JUN-2000; 2000WO-US18152.

XX 30-JUN-1999; 99US-0345468.
 XX 06-DEC-1999; 99US-0454824.
 XX 14-FEB-2000; 2000US-0503387.

XX (MILL-) MILLENNIUM PHARM INC.

XX Busfield SJ, Villette J, Jandrot-Perrus M, Vainchenker W, Gull DS;
 XX Qian DM, Kingsbury G;
 XX MPI: 2001-030877/09.
 XX N-PSDB; AAF29487.

XX New genes encoding human platelet-expressed collagen receptor,
 XX glycoprotein VI, and its modulators, useful for preventing, treating
 XX and diagnosing hemorrhagic disorders, thrombotic diseases and
 XX immunological disorders.

XX Disclosure; Page 217; 227pp; English.

XX The present sequence is given in a specification relating to an isolated
 XX nucleic acid molecule encoding a platelet membrane glycoprotein receptor
 XX glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
 XX and polypeptides and their modulators, e.g. antisense nucleic acids,
 XX ribozymes and antibodies, are useful for preventing, treating and
 XX diagnosing disorders associated with aberrant expression or activity of
 XX GPVI. These disorders include bleeding disorders
 XX (e.g. thrombocytopenia), blood vessel injury, thrombotic disorders
 XX (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
 XX disorders, coronary artery and cerebral artery diseases (e.g. stroke and
 XX ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
 XX infarction), immunological diseases (e.g. platelet disorder) and
 XX embryonic liver disorders. Preferably they are used to prevent acute
 XX cardiac ischaemia following angioplasty and metastatic cancers.
 XX especially of the colon and liver.

XX Sequence 339 AA:

XX Query Match 99.7%; Score 1300; DB 22; Length 339;
 XX Best Local Similarity 99.6%; Pred. No. 7.8e-105;
 XX Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CQGLPRLKSLQALSSLPVLEKPYTLKCCGPGVDLYRLKELSSRRYQDQAVYFIPIPMKR 60
 DB 2 CQGLPRLKSLQALSSLPVLEKPYTLKCCGPGVDLYRLKELSSRRYQDQAVYFIPIPMKR 60
 QY 61 SLAARYRCSYNGSLMSLPDQLFLVATGVFAKSLSAQEPGPAVSSGGVTLCCCTCYG 120
 DB 81 SLAARYRCSYNGSLMSLPDQLFLVATGVFAKSLSAQEPGPAVSSGGVTLCCCTCYG 140
 QY 121 DQFALYKSGDPAPIKPKPRMWRASFPITITVAASGYRCYFSSGDDPYIWSAPDELEL 180
 DB 141 DQFALYKSGDPAPIKPKPRMWRASFPITITVAASGYRCYFSSGDDPYIWSAPDELEL 200

QY 181 VWTGTSVTPSRPLTFEPSSVAEFSAAELTVSEFTNKVFTTETSRITTSKESDSPAGP 240
 DB 201 VWTGTSVTPSRPLTFEPSSVAEFSAAELTVSEFTNKVFTTETSRITTSKESDSPAGP 260
 QY 241 ARQYTTKGN 249
 DB 261 ARQYTTKGN 269
 RESULT : 5
 AB011239
 ID ABU11239 standard; Protein; 339 AA.
 AC ABU11239;
 XX 06-FEB-2003 (first entry)
 DE Glycoprotein VI associated protein sequence #1.
 XX Human; mouse; variable heavy; VH; antigen; cancer;
 XX complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
 XX TANGO 268; extracellular matrix; collagen; platelet release;
 XX proliferation; migration; embryogenesis; inflammation; thrombosis;
 XX degranulation; thrombocytopenia; antibody; thrombotic disorder;
 XX cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
 XX leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
 XX cardiovascular disease; angina pectoris; myocardial infarction;
 XX coronary restenosis; atherosclerosis; immunological disorder;
 XX developmental disorder; embryonic disorder; liver disorder;
 XX cerebral vascular disease; venous thromboembolism disease.

XX Homo sapiens.

XX WO200280968-A1.
 XX 17-OCT-2002.
 XX 09-APR-2002; 2002WO-US11122.
 XX 09-APR-2001; 2001US-0929495.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Busfield SJ, Villette J, Jandrot-Perrus M, Vainchenker W, Gull DS;
 XX Qian DM, Kingsbury G;
 XX MPI: 2003-058477/05.

XX Novel substantially purified antibody immunospecifically binding to
 XX TANGO 268 antigen, useful for treating bleeding disorders such as
 XX thrombocytopenia, stroke, ischaemia, pulmonary embolism, atherosclerosis
 XX -
 XX Disclosure; Page 222-223; 236pp; English.

XX This invention relates to a novel purified antibody comprising a
 XX variable heavy (VH) complementarity determining region (CDR1, VH CDR2
 XX or VH CDR3; or variable light (VL) CDR1, VL CDR2 or VL CDR3, and
 XX immunospecifically binding to a TANGO 268 (also referred as glycoprotein
 XX VI (GPVI)) antigen. The antibodies of the invention act to decrease or
 XX block TANGO 268 binding to extracellular matrix components, or as a
 XX collagen or platelet release and aggregation blocker. The antibodies of
 XX the invention are useful for modulating proliferation, migration,
 XX morphology, differentiation and/or function of megakaryocytes and
 XX platelets, including during development e.g. embryogenesis, modulating
 XX leukocyte-platelet and platelet-endothelium interactions in
 XX inflammation and/or thrombosis, and modulating platelet aggregation and
 XX degranulation. They are also useful for modulating disorders associated
 XX with abnormal or aberrant megakaryocyte and/or platelet proliferation,
 XX migration, morphology, differentiation and/or function, e.g. bleeding
 XX disorders such as thrombocytopenia. Other diseases which may be
 XX modulated by these antibodies are thrombotic disorders, cerebral
 XX vascular diseases (e.g. stroke and ischaemia) venous thromboembolism

CC diseases (e.g., diseases involving leg swelling, pain and ulceration,
CC pulmonary embolism, etc.); coronary diseases (e.g., cardiovascular
CC diseases including angina pectoris, myocardial infarction, coronary
CC revascularization, atherosclerosis, etc.); immunological disorders,
CC rheumatism, arteriosclerosis, embryonic disorders, liver disorders, cerebral
CC vascular disorders, venous thromboembolism disease, coronary diseases,
CC and metastatic cancers. The thrombotic disorder of the invention only causes a
CC transient decrease in platelet counts, platelet aggregation, and/or
CC platelet activation and so have some advantages over prior art
CC methods. The present sequence represents a protein sequence used to
CC create the antibodies of the invention.
CX

SQ Sequence 339 AA;

Query Match	55.7%	Score	1305	DB 24	length	339			
Best Local Similarity	99.6%	Pred. No.	7.5e-105						
Matches	248	Conservative	0	Mismatches	1	Indels	0	Gaps	0

Cy	QSEPLKRPSTJALPSSLVYLEKPVTLRCQSGFGVJLYLEKSSSRYPGDQVLFIPKKR	60
Cy	QSEPLKRPSTJALPSSLVYLEKPVTLRCQSGFGVJLYLEKSSSRYPGDQVLFIPKKR	60
Db	QSEPLKRPSTJALPSSLVYLEKPVTLRCQSGFGVJLYLEKSSSRYPGDQVLFIPKKR	80
Cy	SLAGRRRCSTYONCSLMSLPDQLEJYATVPKPKLSLQPGPAVSSGSDVTLQOQTGYGF	120
Db	SLAGRRRCSTYONCSLMSLPDQLEJYATGVFPKPLSLQPGPAVSSGSDVTLQOQTGYGF	140
Cy	DOEALYKGGPAPYKQPKSRWYRASPFTVTVAHSGITRYCSFSSGRDPLYLMSASDPEL	160
Db	DOEALYKGGPAPYKQPKSRWYRASPFTVTVAHSGITRYCSFSSGRDPLYLMSASDPEL	200
Cy	VYTGTSVTPSRRLPTPEPSSVAESEAETALTYVSTNKKPFTETSKSLTTSKESLSPAGP	240
Db	VYTGTSVTPSRRLPTPEPSSVAESEAETALTYVSTNKKPFTETSKSLTTSKESDSPAGP	260
Cy	ARQYTKGN 249	
Db	ARQYTKGN 269	

Search completed: November 10, 2003, 06:16:57
Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 10, 2003, 06:14:09 ; Search time 17 Seconds

(without alignments)
688.803 million cell updates/sec

Title: US-09-503-387-9
Perfect score: 1304
Sequence: 1 QSGSLPKPSQALPSS-VPL.....SPKSSDPAAPARYTXXN 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026735 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	333	25.5	387	1 K3S1_HUMAN	Q14943 homo sapien
2	322	24.7	304	1 K2S2_HUMAN	P43631 homo sapien
3	320.5	24.6	444	1 K3J1_HUMAN	P43629 h killer ce
4	315	24.2	304	1 K2S1_HUMAN	Q14954 homo sapien
5	314	24.1	304	1 K2S4_HUMAN	P43632 homo sapien
6	314	24.1	348	1 K2L1_HUMAN	P43626 h killer ce
7	314	24.1	348	1 K2L2_HUMAN	P43627 homo sapien
8	312.5	24.0	341	1 K2L3_HUMAN	P43628 h killer ce
9	306.5	23.5	304	1 K2S5_HUMAN	Q14953 homo sapien
10	302	23.2	335	1 G49B_MOUSE	Q64281 mus musculu
11	299	22.9	287	1 FCAR_HUMAN	P24071 homo sapien
12	299	22.9	377	1 K2L4_HUMAN	Q99706 homo sapien
13	297.5	22.8	304	1 K2S3_HUMAN	Q44952 homo sapien
14	294.5	22.6	455	1 K3J2_HUMAN	P43630 homo sapien
15	280	21.5	303	1 G49A_MOUSE	Q61450 mus musculu
16	143.5	11.0	495	1 A1B3_HUMAN	P04217 homo sapien
17	136	10.4	291	1 DM43_D1MR	P82957 didelphis m
18	126.5	9.7	3707	1 PGBM_MOUSE	Q05793 mus musculu
19	123.5	9.5	267	1 FC63_RAT	P27645 ratus norv
20	113.5	8.7	1284	1 NRCA_CHICK	P25331 gallus gall
21	111.5	8.6	4391	1 PGBM_HUMAN	P98160 homo sapien
22	108	8.3	341	1 FC62_CAVPO	Q60513 canis porce
23	107	8.2	261	1 FC63_MOUSE	P88508 mus musculu
24	106	8.1	285	1 FC62_RAT	Q61223 ratus norv
25	105.5	8.1	330	1 FC62_MOUSE	P88101 mus musculu
26	101	7.7	1709	1 SN_HUMAN	Q92222 homo sapien
27	101	7.7	3375	1 UN52_CAEEL	Q65561 caenorhabd-
28	100	7.7	257	1 FC6A_HUMAN	P22319 homo sapien
29	100	7.7	1367	1 AMYH_YEAST	P28640 saccharomyc
30	99.5	7.6	727	1 PECT_MOUSE	Q08481 mus musculu
31	99	7.6	739	1 VCAL_HUMAN	P19320 homo sapien
32	98.5	7.6	3149	1 TEGU_EBV	P31566 epstein-bar
33	97.5	7.5	296	1 FC62_BOVIN	Q28110 bos taurus

34	96.5	7.4	404	1 FC61_MOUSE	P26151 mus musculu
35	96.5	7.4	1694	1 SN_MOUSE	Q62230 mus musculu
36	96	7.4	2774	1 VAPB_RAT	P34926 ratus norv
37	95.5	7.3	348	1 K1LO_RAT	Q92018 ratus norv
38	95.5	7.3	2282	1 ZAN_RABIT	P57999 oryctolagus
39	95	7.3	663	1 SEPI_SCHPO	Q43058 schizosacch
40	95	7.3	739	1 VCAL_MOUSE	P29533 mus musculu
41	94.5	7.2	770	1 DAB2_HUMAN	P98082 homo sapien
42	94.5	7.2	912	1 ICAS_RABIT	Q28730 oryctolagus
43	94.5	7.2	1051	1 PTK7_CHICK	Q91048 gallus gall
44	94.5	7.2	1443	1 NEOL_CHICK	Q90610 gallus gall
45	94	7.2	372	1 Y906_MYCTU	Q10562 mycobacteri

ALIGNMENTS

```

RESULT 1
ID      K3S1_HUMAN      STANDARD:      PRT:      387 AA.
AC      Q14943
DT      01-NOV-1997 (rel. 35, Created)
DT      01-NOV-1997 (rel. 35, Last sequence update)
DT      15-SEP-2003 (rel. 42, Last annotation update)
DE      Killer cell immunoglobulin-like receptor 3D51 precursor (MHC class I
DE      NK cell receptor) (Natural killer killer associated transcript 10) (NKAT-10).
CK      KIR3DS1; OR NKAT10.
CS      Homo sapiens (Human).
CC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX      NCBI_Taxid:9606;
RM      (1)
RP      SEQUENCE FROM N.A.
RX      MEDLINE:96270004; PubMed:8662091;
RA      Coenig C., Samaridis C., Colonna X.;
RT      "Alternative-y spliced forms of human killer inhibitory receptors.";
RL      Immunogenetics 44:227-230(1996).
RM      (2)
RP      VARIANT HIS-166.
RX      MEDLINE:98090086; PubMed:9430221;
RA      Ueberberg X., Vallance N.M., Shum B.P., Shilling H.G.,
RA      Lienert-Weidenbach K., Corliss B., Yan D., Lanter L.L., Parham P.;
RT      "Human diversity in killer cell inhibitory receptor genes.";
RL      Immunity 7:753-763(1997).
CC      - FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC      DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC      - SUBCELLULAR LOCATION: Type I membrane protein.
CC      - SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC      - SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL: L76661; AAB36589.1; -
CC      R5SP: P43626; INKR.
CC      Genew: HGNC:6340; KIR3DS1.
CC      NM_: 604957; -
CC      DR      GO: GO:0005887; C: integral to plasma membrane; NAS.
CC      DR      GO: GO:001993; F: defense/immunity protein activity; NAS.
CC      DR      GO: GO:0030106; F: MHC class I receptor activity; NAS.
CC      DR      GO: GO:0060955; P: immune response; NAS.
CC      DR      GO: GO:0036101; P: natural killer cell activation; NAS.
CC      InterPro: IPR003599; Ig.
CC      InterPro: IPR003006; Ig_MHC.
CC      Pfam: PF00047; Ig_3.
CC      SMART: SM00409; Ig_3.
CC      PROSITE: PS00855; IG_LIKE; FALSE_NEG.
CC      Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW

```

Repeat: Multigene family: Polymorphism.
 FT SIGNAL 1 BY SIMILARITY.
 FT CHAIN 22 387 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
 FT 3DS1.
 FT DOMAIN 22 340 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 341 360 POTENTIAL.
 FT DOMAIN 361 387 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 42 402 IG-LIKE C2-TYPE 1.
 FT DOMAIN 137 302 IG-LIKE C2-TYPE 2.
 FT DOMAIN 237 300 IG-LIKE C2-TYPE 3.
 FT DISULFID 49 95 BY SIMILARITY.
 FT DISULFID 144 195 BY SIMILARITY.
 FT DISULFID 244 293 BY SIMILARITY.
 FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 166 166 R -> H.
 FT /FTID=VAR 010377.
 SQ SEQUENCE 387 AA: 42902 MW: 0875CE73D1D1E100 CRC64:
 Query Match 25.5%; Score 333; DB 1; Length 387;
 Best Local Similarity 37.3%; Pred. No. 5,2e-19;
 Matches 90; Conservative 26; Mismatches 91; Indels 34; Gaps 7;
 QY 7 KPSIQALPSLVPLKPYTLRQCGPGVDLYRLEK----LSSRYQDQ-----AVLF1 55
 Db 123 KPSILAHGPJVKSGEVIILQCMWDIHFHFLEKEMISKPSRLVQIHGVSKANFSI 182
 QY 56 PAMKRSIAGRYRC-----SYNGSLMSLPSDQLVLVATGVFAKPSLSAQPGPAVSSG 108
 Db 183 GSMWRALAGTYRCGVSTHTPYQ----LSAPSDPLDLYVTGVLKPSLSAQPGPKVQAGS 219
 QY 109 DVLIOCCYRIGFDQFALYKGDPAFYKNP-----ERYKRASFPITVTAAHSGTYRCYSF 163
 Db 239 SVTLSCSSRSYDYVHLSREGGAEERLPAVKRYRTFQADFL--GPATHGCTYRCFGS 296
 QY 164 SSRAPYMSAPSDQLVLVATGVSTYPSRLPREPSSVAEFS-----ATAEVYSPFNKY 219
 Db 297 FRHSPEYSPSDPLVSTGNPSSWPSPSPSSKGNLRHHLIGTSVVKIPFTILL 356
 QY 219 F 219
 Db 357 F 357
 RESULT 2
 K2S2 HUMAN STANDARD; FRT; 304 AA.
 ID K2S2 HUMAN
 AC P43631; 014955;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Killer cell immunoglobulin-like receptor 2B2 precursor (KHC class 2
 DE NK cell receptor) (Natural killer associated transcript 5) (KXAT-5)
 DE [p58 natural killer cell receptor clone Cc-49] (p58 NK receptor) (NK
 DE receptor 183 Act1).
 OS KIR2DS2 OR NKAT5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCB1_Taxid=9606;
 RN 11
 RP SEQUENCE OF 2-304 FROM K.A.
 RC TISSUE=Natural killer cells;
 RX MEDLINE=95269128; PubMed=77439980;
 RA Wagtmann N., Blasson R., Cantoni C., Verdiani S., Malnati M.S.,
 RA Vitale M., Bottino C., Moretta L., Moretta A., Long E.O.;
 RT "Molecular clones of the p58 NK cell receptor reveal immunoglobulin-
 RT related molecules with diversity in both the extra- and intracellular
 RT domains";
 RL Immunity 2:439-449(1995).
 RP SEQUENCE FROM N.A.

RX MEDLINE=95269128; PubMed=7716543;
 RA Colonna M., Samadpour J.;
 RT "Cloning of immunoglobulin-superfamily members associated with HLA-C
 RT and HLA-B recognition by human natural killer cells";
 RN Science 268:405-408(1995).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphoid;
 RX MEDLINE=96195217; PubMed=8627176;
 RA Blasson R., Cantoni C., Falco M., Verdiani S., Bottino C., Vitale M.,
 RA Conte R., Poggi A., Moretta A., Moretta L.;
 RT "The human leukocyte antigen (HLA)-C-specific 'activatory' or
 RT 'inhibitory' natural killer cell receptors display highly homologous
 RT extracellular domains but differ in their transmembrane and
 RT intracytoplasmic portions";
 R. Exp. Med. 183:645-656(1996).
 CC FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
 CC - FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
 CC DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
 CC - SUBCELLULAR LOCATION: type 1 membrane protein.
 CC - SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC - SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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 CC
 DR EMBL: U24079; AAC50338.1; ALT_INT.
 DR EMBL: L41347; AA65225.1; -.
 DR EMBL: X89893; CAA61983.1; -.
 DR HSSP: P43626; INKR.
 DR Genew: HGNC:6334; KIR2DS2.
 DR MIM: 604953; -.
 DR GO: GO:0016021; C: integral to membrane; NAS.
 DR GO: GO:0034888; F: transmembrane receptor activity; NAS.
 DR GO: GO:0006955; P: immune response; NAS.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; IG_2.
 DR SMART: SM00409; IG_1.
 DR PROSITE: PS00835; IG_LIKE; FALSE_NEG.
 DR Receptor: Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
 KW Repeat; Multigene family.
 FT SIGNAL 1
 FT CHAIN 22 304 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
 FT 2DS2.
 FT DOMAIN 22 245 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 246 265 POTENTIAL.
 FT DOMAIN 266 304 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 42 107 IG-LIKE C2-TYPE 1.
 FT DOMAIN 142 205 IG-LIKE C2-TYPE 2.
 FT DISULFID 49 100 BY SIMILARITY.
 FT DISULFID 149 198 BY SIMILARITY.
 FT CARBOHYD 84 94 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 20 20 W -> G (IN REF. 3).
 SQ SEQUENCE 304 AA: 186C77DD9E86A28 CRC64:
 Query Match 24.7%; Score 322; DB 1; Length 304;
 Best Local Similarity 33.6%; Pred. No. 2,8e-18;
 Matches 93; Conservative 32; Mismatches 94; Indels 59; Gaps 10;
 QY 7 KPSIQALPSLVPLKPYTLRQCGPGVDLYRLEKSSRYQD-----QAVL 53
 Db 28 KPSILAHGPJVKSGEVIILQCMWDIHFHFLEKEMISKPSRLVQIHGVSKANFSI 85
 QY 54 PAMKRSIAGRYRC-----SYNGSLMSLPSDQLVLVATGVFAKPSLSAQPGPAVSS 106
 Db 86 SIGPMWMDIAGTYRCGVSTHTPYQ----LSAPSDPLDLYVTGVLKPSLSAQPGPTVLA 141

Qy 107 GSDTLQCTRYGDDQALVYKESD-----PAPYKPERMYRASPIITVTAAHSTIR 159
Dy 142 GESVTLSSSSSSSYDMWH--SREGAEHRRFSAGKXVGT--FOADFLL--GPAIHGQTVR 197
Qy 160 CYSRSSRDPYLMASPDPLELVGTSTVTPERLPTPEPSSVAERSE-----ATAELTVSF 214
Db 198 CFSGRDPSFYEMWSSSDPLVSTGNNSNENFSTPESSSKTGNRHLHLVIGISVYKIPF 257
Qy 215 T-----NK-----VFTTSTRSITTSPESD 235
Db 258 TILFPLLRWCSNKKNAAVVDCBPACNRTVNSCSD 294

RESULT 3
K3--HUMAN
AC K3L1 HUMAN STANDARD; PRT; 444 AA.
AC P43629; Q43473; Q16541;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Killer cell immunoglobulin-like receptor 30L precursor (MHC class I
DE NK cell receptor) (Natural killer associated transcript 3) (NKAT-3)
DE (p70 natural killer cell receptor clones Cc-2/CL-11) (HLA-B*44 specific
DE inhibitory NK cell receptor).
CN KIR3DL1 OR NKAT3 OR NK31.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCBI_TaxID=9606;
CX (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Natural killer cells;
RX MEDLINE=95232526; PubMed=7716543;
RA Cloning of immunoglobulin-superfamily members associated with HLA-C
R- and HLA-B recognition by human natural killer cells.";
RT Science 268:405-408(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood lymphocytes;
RX MEDLINE=96111957; PubMed=877725;
RA Wagtmann N., Rajagopalan S., Winter C.C., Peruzzi M., Long E.C.;
RT "Killer cell inhibitory receptors specific for HLA-C and HLA-B
RT identified by direct binding and by functional transfer.";
RL Immunity 3:801-809(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood lymphocytes;
RX MEDLINE=96343861; PubMed=8760804;
RA Pende D., Biassoni R., Cantoni C., Verdiani S., Falco M.,
RA di Donato C., Accame L., Bottino C., Moretta A., Moretta L.;
RT "The natural killer cell receptor specific for HLA-A allotypes: a
RT novel member of the p58/p70 family of inhibitory receptors that is
RT characterized by three immunoglobulin-like domains and is expressed
RT as a 140-kD disulphide-linked dimer.";
RL J. Exp. Med. 184:505-518(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95378652; PubMed=7650366;
RA D'Andrea A., Chang C., Franz-Bacon K., McClanahan T., Phillips C.H.,
RA Lanier L.L.;
RT "Molecular cloning of NKBL, A natural killer cell receptor for HLA-B
RT allotypes.";
RL J. Immunol. 155:2306-2310(1995).
RN [5]
RP SEQUENCE FROM N.A., AND VARIANTS.
RX MEDLINE=96090886; PubMed=9436221;
RA Chisberg M., Valiante N.M., Stuck R.P., Snilling R.G.,
RA Lienert-Waldenbach K., Collins B., Ryan D., Lanier L.L., Pathan P.;
RT "Human diversity in killer cell inhibitory receptor genes.";
RL Immunity 7:751-763(1997).

CC - FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA B*4
CC ALLELE INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING
CC CELL LYSIS.
CC - SUBCELLULAR LOCATION: Type I membrane protein.
CC - SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC - SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC
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CC
CC EMBL: J01269; AAA69870.1; -
CC EMBL: J01273; AAB52521.1; -
CC EMBL: J0274; AAB52522.1; -
CC EMBL: X94262; CAA63938.1; -
CC EMBL: U31416; AAC33725.1; -
CC EMBL: AF022049; AAB95322.1; -
CC F01; G01925; G01925.
CC HSSP; P43626; INKR.
CC Genes; HGNC:6338; KIR3DL1.
CC MIM: 604946; -
CC GO: GO:0035887; C:integral to plasma membrane; NAS.
CC GO: GO:0003793; F:defense/immunity protein activity; NAS.
CC GO: GO:0030109; F:HLA-B specific inhibitory MHC class I recep. . . NAS.
CC GO: GO:0006955; P:immune response; NAS.
CC GO: GO:0030102; P:negative regulation of natural killer cell . . . NAS.
CC InterPro; IPR003599; Ig.
CC InterPro; IPR003006; IG_YHC.
CC Pfam; PF00647; Ig_3.
CC SMART; SM00409; IG_3.
CC PROSITE; PS50835; IG_LIKE; FAUSE NEG.
CC KX Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
CC Repeat; Multigene family; Polymorphism.
CC SIGNAL 1 21
CC CHAIN 22 444
CC
CC DOMAIN 22 340 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 341 360 POTENTIAL.
CC DOMAIN 361 444 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 42 102 IG-LIKE C2-TYPE 1.
CC DOMAIN 137 202 IG-LIKE C2-TYPE 2.
CC DOMAIN 237 360 IG-LIKE C2-TYPE 3.
CC DISULFID 49 95 BY SIMILARITY.
CC DISULFID 144 195 BY SIMILARITY.
CC CARBOHYD 244 293 BY SIMILARITY.
CC CARBOHYD 179 179 N-LINKED (G-CNAC. . .) (POTENTIAL).
CC CARBOHYD 273 273 N-LINKED (G-CNAC. . .) (POTENTIAL).
CC VARIANT 2
CC
CC VARIANT 13 13 L -> F.
CC VARIANT 23 23 /FTID=VAR_010320.
CC VARIANT 23 23 /FTID=VAR_010321.
CC VARIANT 68 68 I -> V.
CC VARIANT 75 75 /FTID=VAR_010322.
CC VARIANT 259 259 G -> R.
CC VARIANT 333 333 /FTID=VAR_010326.
CC VARIANT 333 333 S -> C.
CC
CC SEQUENCE 444 AA; 49098 NM; 47DEAI2BBAFDECS3 CRC64;
CC
CC Query Match: 24.6%; Score 320.5; DB: Length 444;
CC Best Local Similarity: 38.6%; Pred. No. 5.9e-18;
CC Matches 83; Conservative 22; Mismatches 81; Indels 23; Gaps 5;
CC
CC 7 KPSLQALPSSLVPEKPVTLRCGPPGVLYRLKLTSSSRVODQAV-----LFI 55

FN [2].
RX MEDLINE=96270004; PubMed=866291,
RA Deshing C., Satharidis V., Colonna M.;
RT "Alternatively spliced forms of human killer inhibitory receptors.";
RL Immunogenetics 44:227-230(1996).
RN {3}
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RX MEDLINE=9635503; PubMed=8765026;
RA Bottino C., Sivori S., Vitale M., Cantoni C., Falco M., Perde D.,
RA Moretta L., Avigiani R., Semenzato G., Blasson R., Moretta L.,
RA Moretta A.;
RT "A novel surface molecule homologous to the p58/p50 family of
RT receptors is selectively expressed on a subset of human natural
RT killer cells and induces both triggering of cell functions and
RT proliferation.";
RL Eur. J. Immunol. 26:1816-1824(1996).
RN {4}
RP SEQUENCE FROM N.A.
RA Chan H.W., Salter R.D.;
RC Submitted (MAY-1997) to the EMBL/Genbank/DDJ databases.
CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLIELES.
CC DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC -1- SUBCELLULAR LOCATION: type 1 membrane protein.
CC -1- SIMILARITY: BELONGS TO THE LYMPHOGLUBULIN SUPERFAMILY.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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CC -----
DR EMBL: U24077; AAC50336.1; ALT_INT.
DR EMBL: L76671; AB36599.1; -.
DR EXBL: X94609; CA64317.1; -.
DR EXBL: AF032255; AA61281.1; -.
DR HSSP: P43326; INKR.
DR GeneW: HGNC:6336; XR2D54.
DR MIM: 604955; -.
DR GO: GO:0005887; C:integral to plasma membrane; TAS.
DR GO: GO:0003822; F:MHC-interacting protein; TAS.
DR InterPro: IPR003599; IG.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; IG_2.
DR SMART: SMC0409; IG_1.
DR PROSITE: PS00835; IG_LIKE; FALSE NEG.
KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW Repeat; Multigene family.
KM SIGNAL 1 21
FT FT 22 304
FT CHAIN 1 21
BY SIMILARITY.
KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
DS4.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
BY SIMILARITY.
N-LINKED (GLCNAc . . .) (POTENTIAL).
N-LINKED (GLCNAc . . .) (POTENTIAL).
N-LINKED (GLCNAc . . .) (POTENTIAL).
N-LINKED (GLCNAc . . .) (POTENTIAL).
N-LINKED (GLCNAc . . .) (POTENTIAL).
N-LINKED (GLCNAc . . .) (POTENTIAL).
N-LINKED (GLCNAc . . .) (POTENTIAL).
CEBPAF3FDF679A3F CRC64;
SEQUENCE 304 AA: 33583 MW:
SEQUENCE

Query Match	24.1%	Score 314	D3 1	Length 304
Best Local Similarity	36.3%	Pred. No. 1 2e-17		
Matches 90	Conservative	30	Mismatches 92	Indels 36
			Gaps	9

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CY  QSGPLPKPQLQPLSPSLVPLEKPYTLRQCGPGVD--LVRLKELSSSRV-----QC 44
Db  QCEVHKRKEFLPLPGHVLKSEBETVILQCMQVMEHFLLRKGFNNITLHLIGEHHDGV 81
CY  50 QAVLFIPAKKSLAGRYRC-----SYQNSLWLSPPDQLELVATGVAPKPSLSAQPGP 102
Db  82 KNMFSGIPKMPPLAAGTGYRCYCGVSPHSYPQ----LSAPSDPLDMVILLYKPSLSAQPGP 137
CY  103 AVASGGSDVTLCCOTRGFGQFALVYEGGPADYKNP-----ERWRASGFPIITVFAASGT 157
Db  136 TWAGAGNTVLTSSSSASSTDMYTLSEEGAMHRRLPAYRSINGTGADPPL--GRATHGCT 195
CY  158 YRCYSSFSRD--PYLWSAPSDPLELVITGTVTPSRLPTEPPSSVAEFS-----ATNELT 211
Db  196 YRCFG--SPFDAPAYEMNSQSDPLVAVTGTPNPSPNSWSPTEPFSKTKGNFRHLVLTGSVVK 254
CY  212 VSTFNKVF 219
Db  255 IPEITLLP 262

RESULT 6
XZL1_HUMAN
ID XZL1_HUMAN STANDARD: PRT: 348 AA.
AC P43626; O43470;
CT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DI 15-SEP-2003 (Rel. 42, Last annotation update)
DE Killer cell immunoglobulin-like receptor 2D11 precursor (MHC class I
DE NK cell receptor) (Natural killer receptor associated transcript 1) (NKAT-1)
DE (p58 natural killer cell receptor clones CU-42/47.1) (p58 NK
DE receptor) (p58.1 MHC class-I specific NK receptor).
DE KIR2DL1 OR NKAT1 OR CD158A.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX KCP1_TaxID=9606;
EK (1)
RK SEQUENCE FROM N.A.
RC TISSUE=Natural killer cells;
RX MEDLINE=95232526; PubMed=7716543;
RA Colonna M., Samaridis J.;
RT "Cloning of immunoglobulin-superfamily members associated with HLA-C
RT and HLA-B recognition by human natural killer cells.";
RL Science 268:405-408(1995).
RN
RN SEQUENCE FROM N.A., AND SEQUENCE OF 22-45.
RP TISSUE=Natural killer cells;
RC MEDLINE=95269128; PubMed=7749980;
RA Wactmann N., Bassoni R., Cantoni C., Verdiani S., Maini M.S.,
RA Liebert-Weidenbach K., Corliss B., Ryan D., Lanier L.L., Parham P.;
RA "Human diversity in killer cell inhibitory receptor genes.";
RL Immunity 7:753-763(1997).
RN
RN [4]
RX X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 27-221.
RP MEDLINE=97433335; PubMed=9286975;
RA Fan Q.R., Nossyak L., Winter C.C., Wagtmann N., Long E.O., Wiley D.C.;
RA "Structure of the inhibitory receptor for human natural killer cells
RA resembles haematopoietic receptors.";
RT Native 389:96-100(1997).
CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING CELL LYSIS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein
CC -1- SIMILARITY: BELONGS TO THE IMMOGLOBULIN SUPERFAMILY.

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AC      P43628: 043472;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Killer cell immunoglobulin-like receptor 2DL3 precursor (MHC class I
DE      NK cell receptor) (Natural killer associated transcript 2) (NKAT-2)
DE      (p58 natural killer cell receptor clone Cl-6) (p58 NK receptor) (p58.2
DE      MHC class-I specific NK receptor).
CN      KIR2DL3 OR NKAT2 OR CD158b.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
CX      NCBI_Taxid:9606;
[1]
RN      R2
RS      SEQUENCE FROM N.A.
RC      TISSUE=Natural killer cells;
RX      MEDLINE=95232526; PubMed=7716543;
RX      Colonna M., Samaridis C.;
RX      "Cloning of immunoglobulin-superfamily members associated with HLA-C
RX      and HLA-B recognition by human natural killer cells.";
RL      Science 268:405-408(1995).
[2]
RN      R3
RS      SEQUENCE FROM N.A.
RC      TISSUE=Natural killer cells;
RX      MEDLINE=95269128; PubMed=7749980;
RX      Westermann N., Bissont F., Carton C., Verdiani S., Malnati M.S.,
RX      Vitale M., Bottino C., Moretta L., Moretta A., Long E.O.;
RX      "Molecular clones of the p58 NK cell receptor reveal immunoglobulin-
RX      related molecules with diversity in both the extra- and intracellular
RX      domains".
RL      Immunity 2:439-449(1995).
[3]
RN      R4
RS      SEQUENCE FROM N.A., AND VARIANTS ALA-9; ARG-32; GLY-56; ARG-71 AND
RN      HIS-318.
RX      MEDLINE=96090086; PubMed=3430221;
RX      Unberg N., Vallian N.M., Shum B.P., Shilling H.G.,
RX      Liener-Waidenbach K., Corlies B., Ryan D., Lanier L., Fathian P.;
RX      "Human diversity in killer cell inhibitory receptor genes.";
RL      Immunity 7:753-763(1997).
RT      RL
RS      FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC      THIS IS THE ACTIVITY OF NK CELLS THUS PREVENTING CELL LYSIS.
CC      -1- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC      -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC      -----
CC      CC
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CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL; LA1268; AAA69869.1; -
DR      EMBL; U24074; AAC50333.1; -
DR      EMBL; AF622048; AAB95321.1; -
DR      PIR; I61725; I61725.
DR      HSSP; P43626; INKR.
DR      Genew; HGNC:6331; KIR2DL3.
DR      MIM; 604938; -
DR      GO; GO:0016021; C:integral to membrane; TAS.
DR      GO; GO:0004872; F:receptor activity; TAS.
DR      GO; GO:0006955; P:immune response; TAS.
DR      InterPro; IPR003599; IG_MHC.
DR      InterPro; IPR003006; IG_MHC.
DR      Pfam; PF00047; Ig; 2.
DR      SMART; SM00409; IG; 1.
DR      PROSITE; PS50835; IG_LIKE; FALSE NEG.
KW      Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW      Repeat; Multigene family; Polymorphism.
FT      SIGNAL 1 21 BY SIMILARITY.
FT      CHAIN 22 341 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT      2DL3.

```



```

RT "Cloning of the gp49B gene of the immunoglobulin superfamily and
RT demonstration that one of its two products is an early-expressed mast
RT cell surface protein originally described as gp49."
RL J. Biol. Chem. 269:8393-8401(1994).
CC -1- FUNCTION: MAY PLAY A ROLE IN CELL-CELL OR CELL-CYTOKINE
CC INTERACTIONS DURING THE DEVELOPMENT OF MAST CELLS FROM MULTIPOTENT
CC PROGENITORS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=GP49B1;
CC IsoId=Q64281-1; Sequence=Displayed;
CC Name=GP49B2;
CC IsoId=Q64281-2; Sequence=VSP_002510; VSP_002511;
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC
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CC -----
DR EXBL: U05266; AAA17799.1; -
DR EXBL: U05265; AAA17797.1; -
DR EXBL: U05265; AAA17798.1; -
DR EXBL: U05264; AAA17796.1; -
DR FIR: A53434; A53434;
DR FIR: B53434; B53434;
DR HSSP: P43626; INKR.
DR MGD: MGI:102701; Gp49b.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR03006; Ig_MHC.
DR Pfam: PF00047; Ig_2.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Signal; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
KW Alternative splicing.
FT SIGNAL 1 23 BY SIMILARITY
FT CHAIN 24 335 MAST CELL SURFACE GLYCOPROTEIN GP49B.
FT DOMAIN 24 238 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 239 260 POTENTIAL.
FT DOMAIN 261 335 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 125 IG-LIKE C2-TYPE 1.
FT DOMAIN 124 212 IG-LIKE C2-TYPE 2.
FT DISULFID 49 98 POTENTIAL.
FT DISULFID 144 196 POTENTIAL.
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPIC 232 232 G -> D (in isoform GP49B2).
FT VARSPIC 233 271 /FTId=VSP_002510.
FT VARSPIC 271 271 Missing (in isoform GP49B2).
FT VARSPIC 271 271 /FTId=VSP_002511.
SQ SEQUENCE 335 AA; 37544 MW; 6005186D524E7876 CRC64;
Query Match 23.2%; Score 302; DB 1; Length 335;
Best Local Similarity 33.3%; Pred. No. 1.2e-16;
Matches 77; Conservative 36; Mismatches 96; Indels 22; Gaps 5;

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DB 200 FRNEPQVMSKPSNSLHLMISSTK--DQSGTPRE--DGLFTYKILIGVLSVF 247
RESULT 11
FCAR_HUMAN STANDARD; PRT; 287 AA.
ID FCAR_HUMAN Q13603; Q13604; Q15727; Q15728; Q92590;
AC Q1-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Immunoglobulin alpha Fc receptor precursor (Iga Fc receptor) (CD89
DE antigen).
GN FCAR OR CD89.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A.1).
RX MEDLINE=91079769; PubMed=2258698;
RA Malszewski C.R.; March C.C.; Schoenborn M.A.; Gimpel S.; Shen L.;
R Expression cloning of a human Fc receptor for Iga.
RL J. Exp. Med. 172:1665-1672(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM A.1).
RC TISSUE=Bone marrow;
RX MEDLINE=95363085; PubMed=7636188;
RA de Wit T.P.X.; Morton H.C.; Capel P.J.A.; van de Winkel J.G.C.;
R Structure of the gene for the human myeloid Iga Fc receptor (CD89).
RL J. Immunol. 155:1203-1209(1995).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS A.2 AND A.3).
RC TISSUE=Alveolar macrophage; and Monocytes;
RX MEDLINE=96247667; PubMed=8666819;
RA Patry C.; Sibille Y.; Lehen A.; Monteiro R.C.;
R Identification of Fc alpha receptor (CD89) isoforms generated by
RT alternative splicing that are differentially expressed between blood
RT monocytes and alveolar macrophages.
RL J. Immunol. 156:4442-4448(1996).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS B AND B-DELTA-S2).
RA van Dijk T.B.; Morton H.C.; Caldenhoven E.; Bracke M.;
RA Raaijmakers J.A.M.; Lamers J.W.J.; Koederman L.; Groot R.P.;
RL Submitted (May-1996) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM A.3).
RX MEDLINE=96433090; PubMed=8836118;
RA Pleas R.J.; Andrews P.D.; Kerr M.A.; Woolf C.M.;
R "Alternative splicing of the human Iga Fc receptor CD89 in
RT neutrophils and eosinophils."
RL Biochem. J. 318:771-777(1996).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM U02).
RA Toyabe S.; Kuwano Y.; Takeda K.; Uchiyama M.; Abo T.;
R "Alternatively spliced forms of monocyte Iga Fc receptors in patients
RT with Iga nephropathy."
RL Submitted (Sep-1996) to the EMBL/Genbank/DBJ databases.
RN [7]
RP SUBUNIT5.
RX MEDLINE=94375887; PubMed=7522255;
RA Pfefferkorn L.C.; Yeaman G.R.;
R "Association of Iga-Fc receptors (Fc alpha R) with Fc epsilon RI
RT gamma 2 subunits in U937 cells. Aggregation induces the tyrosine
RL phosphorylation of gamma 2."
J. Immunol. 153:3228-3236(1994).
CC -1- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS ALPHA.
CC MEDIATES SEVERAL FUNCTIONS INCLUDING CYTOKINE PRODUCTION.
CC -1- SCENIT: ASSOCIATES WITH THE FC EPSILON RI GAMMA 2 RECEPTOR
CC INDUCING TYROSINE PHOSPHORYLATION OF GAMMA 2.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (FORM A) AND SOLUBLE
CC (FORM B).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=6;

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RA Unreig M., Valiante N.M., Shum B.P., Shilling H.G.,
 RA Lienert-Weidenbach K., Corliss B., Tian D., Lanier L.L., Parham P.,
 RT "Human diversity in killer cell inhibitory receptor genes.",
 RL Immunity 7:753-763(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Chan H.W., Salter R.D.,
 RT "Exon deletion contributes to structural diversity of 2D4 killer
 RT inhibitory receptors.",
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=9723129; PubMed=9359894;
 RA Selvakumar A.,
 RT "Polymorphism and domain variability of human killer cell inhibitory
 RT receptors.",
 RL Immunol. Rev. 155:183-196(1997).
 CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLIELES.
 CC -1- INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING CELL LYSIS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Everct=Alternative splicing; Named isoforms=6:
 CC Name=1;
 CC IsoId=Q99706-1; Sequence=Disp.ayed;
 CC Name=2; Synonyms=AS1;
 CC IsoId=Q99706-2; Sequence=VSP_002609;
 CC Name=3; Synonyms=AS;
 CC IsoId=Q99706-3; Sequence=VSP_002610;
 CC Name=4; Synonyms=ASD1;
 CC IsoId=Q99706-4; Sequence=VSP_002610;
 CC Name=5; Synonyms=ASD2;
 CC IsoId=Q99706-5; Sequence=VSP_002605, VSP_002610, VSP_002611;
 CC Name=6;
 CC IsoId=Q99706-6; Sequence=VSP_002608, VSP_002609, VSP_002610;
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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 CC -----
 DR EMBL; U71139; AA849756.1; -;
 DR EMBL; AF003123; AA861926.1; -;
 DR EMBL; AF003116; AA861926.1; JOINED.
 DR EMBL; AF003117; AA861926.1; JOINED.
 DR EMBL; AF003118; AA861926.1; JOINED.
 DR EMBL; AF003119; AA861926.1; JOINED.
 DR EMBL; AF003121; AA861926.1; JOINED.
 DR EMBL; AF003122; AA861926.1; JOINED.
 DR EMBL; AF003120; AA861926.1; JOINED.
 DR EMBL; AF002979; AA871387.1; -;
 DR EMBL; AF002980; AA871388.1; -;
 DR EMBL; AF002981; AA871389.1; -;
 DR EMBL; AF002982; AA871390.1; -;
 DR EMBL; X97229; CA65868.1; -;
 DR EMBL; X99479; CA67842.1; -;
 DR EMBL; X99480; CA67843.1; -;
 DR EMBL; X99481; CA67844.1; -;
 DR EMBL; AF034771; AA895164.1; -;
 DR EMBL; AF034772; AA895165.1; -;
 DR EMBL; AF034773; AA895166.1; -;
 DR EMBL; AF110035; AAD24763.1; -;
 DR EMBL; AF110032; AAD24763.1; JOINED.
 DR EMBL; AF110033; AAD24763.1; JOINED.
 DR EMBL; AF110034; AAD24763.1; JOINED.
 DR EMBL; U73394; AAC51146.1; -;
 DR Genew; HGNC:6332; KIR2DL4.
 DR MIM; 604945; -;
 GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0004889; F:transmembrane receptor activity; TAS.
 DR GO; GO:0006968; P:cellular defense response; TAS.
 DR GO; GO:0007185; P:signal transduction; TAS.
 DR InterPro: IPR03006; Ig-MHC.
 DR Pfam: PF00047; Ig_2.
 DR PROSITE: PS00835; IG-LIKE; FALSE NEG.
 DR Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
 KW Repeat; Multigene family; Alternative splicing; Polymorphism.
 FT SIGNAL 1 21
 FT CHAIN 22 377
 FT
 FT DOMAIN 22 242
 FT TRANSMEM 243 263
 FT DOMAIN 264 377
 FT DOMAIN 44 104
 FT DOMAIN 139 202
 FT DISULFID 51 97
 FT DISULFID 146 195
 FT CARBOHYD 141 141
 FT CARBOHYD 175 175
 FT VARSPLIC 27 121
 FT VARSPLIC 219 235
 FT VARSPLIC 236 270
 FT VARSPLIC 271 288
 FT VARSPLIC 53 53
 FT VARIANT 87 87
 FT VARIANT 138 138
 FT VARIANT 209 209
 FT VARIANT 271 271
 FT VARIANT 371 371
 FT CONFLICT 229 229
 FT SEQUENCE 377 AA; 41527 MW; 7EC9EC0C7F4143B CRC64;
 Query Match 22.9%; Score 299; DB 1; Length 377;
 Best Local Similarity 34.2%; Pred. No. 2.3e-16;
 Matches 78; Conservative 36; Mismatches 94; Indels 20; Gaps 6;
 QY 3 GPLPKSLALPSSVPLEKPYTRCCGPGVDLYRLELSS-----SFYQDQAVLFI 55
 DB 26 GGQDKPFGCSAMPSAVVPGGHVLRCHTRRGHNIFLYKKDGVPPPELYNRIFFMNSFLS 85
 QY 56 PAKRSLAGRYRC---SYONGSLWSLPDQLELVA-GVPAKPS-SAQPGPAVSSGADVTL 112
 DB 66 P-LTPAHAGTYRCGRHPHSPTFEMSAFSLVIMVGLYKESLTLRPPPTVATGENTVL 144
 QY 113 QCTRYGFPQFALYKGDPAFYPKPR-----EKMYRASFPIITVTAHSGTYRCYSSSRD 167
 DB 145 SCSSQSSFDIYHLRSGEAEHLRLPAVPSINGTFQADFPL--GPAHGETYRCFGSFGHS 202
 QY 168 PYLWASPDPLELVYTGSVTPSRLLPTSP--PSSVAESEATAEITVS 213
 DB 203 PYLWASDPLELVYTGSVTPSGSSWPSFTSPFTGTGIRHLHAIVRIYVA 250
 RESULT 13
 K2S3 HUMAN STANDARD; PRT; 304 AA.
 AC Q14952; Q03644;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)

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DE Killer cell immunoglobulin-like receptor D2S3 precursor (MHC class I
DE NK cell receptor) (Natural killer associated transcript 7) (NKAT-7).
GN KIR2D3 OR NKAT7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96270004; PubMed=8662091;
RA Doebering C., Samaridis J., Colonna M.;
RT "Alternatively spliced forms of human killer inhibitory receptors.";
RL Immunogenetics 44:227-230(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Lymphoid;
RA Blasson R.;
RL Submitted (Apr-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLIELES.
CC DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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CC -----
DR EMBL: L76670; AAB36598.1; -
DR EMBL: X97211; CAA65870.1; -
DR HSSP: P43626; INKR.
DR Genew; HGNC:6335; KIR2D3.
DR MIM: 604954; -
DR GO: GO:0005887; C:intracellular plasma membrane; TAS.
DR GO: GO:0003822; F:MHC-interacting protein; TAS.
DR GO: GO:0006968; P:cellular defense response; TAS.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00447; Ig_2.
DR SMART; SMC0409; Ig_1.
DR PROSITE; PS50835; IG_LIKE; FALSE NEG.
DR Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW Repeat; Multigene family.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 304 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT DOMAIN 22 245 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 246 264 POTENTIAL.
FT DOMAIN 265 304 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 107 IG-LIKE C2-TYPE 1.
FT DOMAIN 142 205 IG-LIKE C2-TYPE 2.
FT DISULFID 49 100 BY SIMILARITY.
FT DISULFID 149 198 BY SIMILARITY.
FT CARBOHYD 67 67 N-LINKED (GLCNAc...) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAc...) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAc...) (POTENTIAL).
SQ SEQUENCE 304 AA: 33717 MW: 8069379844PDE7E CR664;
Query Match: 22.8%; Score 297.5; DB 1; Length 304;
Best Local Similarity 36.5%; Pred. No. 2,3e-16;
Matches 80; Conservative 24; Mismatches 78; Indels 37; Gaps 7;
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QY 7 KSSLQALPSSVPLEKPYLTKROGPGVDYLRLEKSSSRYYD-----QAVL 53
DB 54 F:PAMRSLAGRYRC-----SYQNSLMS--PSDQCELVATGVFAKPSLSAPQPAVSS 106
DB 86 SIGRMRGDLAGTTCRCGVSVPHSFYQ----FSAPSDPLIVITGVYKPSLSAQPPPTVLA 141

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QY 107 GGDVTLQCTRTGFGDFALYKGD-----PAPRKNPRWRASPIITVTAASGTR 155
DB 142 GESVTLTSCSSWSSEYEHJSTEGEAMERFRSAGPKNGT--FGADFPL--GPATGGGTR 197
QY 160 CYFSRRDPYLMASPDPLVWTGTSVPSPLPPEPS 199
DB 198 CFGSFRDPSPEWSKSDPLVSTGTPNSMSPTEPSS 236
RESULT 14
K3L2_HUMAN STANDARD; PRT; 455 AA.
AC P43630; Q13238; Q14947; Q14948; Q92684; Q93657;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Killer cell immunoglobulin-like receptor 3DL2 precursor (MHC class I
DE NK cell receptor) (Natural killer associated transcript 4) (NKAT-4)
DE (p70 natural killer cell receptor clone CL-5).
GN KIR3DL2 OR NKAT4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Natural killer cells;
RX MEDLINE=96111967; PubMed=8777725;
RA Westerman N., Ragovalan S., Winter C.C., Peruzzi M., Long E.O.;
RT "Killer cell inhibitory receptors specific for HLA-C and HLA-B
RT identified by direct binding and by functional transfer.";
RN Immunity 3:801-809(1995).
RN [3]
RP SEQUENCE FROM N.A. AND VARIANT VAL-113.
RX TISSUE=Lymphoid;
RX MEDLINE=96343861; PubMed=8760894;
RX Perde D., Blasson R., Cantoni C., Verdiani S., Falco M.,
RA di Donato C., Accame L., Bottino C., Moretta A., Moretta L.;
RT "The natural killer cell receptor specific for HLA-A allotypes: a
RT novel member of the p58/p70 family of inhibitory receptors that is
RT characterized by three immunoglobulin-like domains and is expressed as
RT a 140-kD disulphide-linked dimer.";
RN J. Exp. Med. 184:505-518(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=96270004; PubMed=8662091;
RA Doebering C., Samaridis J., Colonna M.;
RT "Alternatively spliced forms of human killer inhibitory receptors.";
RN Immunogenetics 44:227-230(1996).
RN [5]
RP VARIANTS ALA-40; VAL-113; ASP-158; HIS-166; PRO-223 AND THR-252.
RX MEDLINE=96090086; PubMed=9430221;
RA Unberg M., Valiante N.M., Shum B.P., Shilling H.G.,
RA Liener-Weldenbach K., Corliss B., Ryan D., Lanier L., Parham P.;
RT "Human diversity in killer cell inhibitory receptor genes.";
RN Immunity 7:753-763(1997).
CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-A ALLIELES.
CC INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING CELL LYSIS.
CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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Dj      92 KFK:RFTASYAGIYNCYXSAGFSEHSDAMELMTGAYENPSLSVFSNWTSGVIS 241
Cy      112 JOCOTRYGFDOPALYKEEDPAPYKPERW-----YRASFPILITVTAASGTYRC 160
Dc      142 FKCSSTLFGRFIIQSG-----KHGLSWTLCQHQANOPTHA:FWLDAVAPNHNCTFRG 196
Cy      161 YFSRSRDPYJMSAPSCPIELVVGTSVTFPRLPTEPPSSVAEFSSEATAEELTVSP 214
Dc      197 YGFENEPQVWSKPSNSJDLMISETK-SQSCPTPE--DGJETYQKILIGVIVSF 247

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Search completed: November 10, 2003, 06:16:04
 Job time : 19 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: November 10, 2003, 06:14:09 ; Search time 35 Seconds

(without alignments)
1835.860 Million cell updates/sec

Title: US-09-503-387-9

Perfect score: 1304
Sequence: 1 QSGPUPKPSLOALPSSLVPL.....SPKSDSPAGAPQYTKGN 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 630525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP_archaea:*
2: SP_bacteria:*
3: SP_fungi:*
4: SP_human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriophage:*
17: SP_archaeal:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1304	100.0	339	4	Q9UIF2	Q9ui12 homo sapien
2	1247	95.6	620	4	Q9HCN6	Q9hcne6 homo sapien
3	1194	91.6	321	4	Q9HCN7	Q9hcnc7 homo sapien
4	424.5	32.6	481	6	Q8M4Z2	Q8mj22 pan troglod
5	419	32.1	447	4	Q8NHJ6	Q8nhj6 homo sapien
6	416	32.1	448	4	O15468	O15468 homo sapien
7	418	32.1	448	4	Q8NHJ5	Q8nhj5 homo sapien
8	418	32.1	448	4	Q8NHJ4	Q8nhj4 homo sapien
9	418	32.1	448	4	Q8NHJ3	Q8nhj3 homo sapien
10	415.5	31.9	631	6	Q8M4Z3	Q8mj23 pan troglod
11	408.5	31.3	645	6	Q8M4Z5	Q8mj25 pan troglod
12	405.5	31.1	631	4	O15471	O15471 homo sapien
13	401	30.8	336	6	Q8S8Q5	Q8s8q5 bos taurus
14	400.5	30.7	631	6	Q75C22	Q75c22 homo sapien
15	400	30.7	631	6	Q8M4Z7	Q8mj27 pan troglod
16	399.5	30.6	491	4	Q8NH70	Q8nh70 homo sapien

17	399	30.6	590	4	O750Z3	O750z3 homo sapien
18	398.5	30.6	489	4	O750I9	O750i9 homo sapien
19	396	30.4	460	6	Q8M4Z4	Q8mj24 pan troglod
20	396	30.4	466	4	Q8NH49	Q8nh49 homo sapien
21	396	30.4	483	4	O750Z0	O750z0 homo sapien
22	393.5	30.2	382	4	Q8NF80	Q8nf80 homo sapien
23	389	29.8	662	6	Q8M4Z6	Q8mj26 pan troglod
24	388.5	29.8	289	4	O750I8	O750i8 homo sapien
25	385.5	29.6	597	4	Q8NHJ8	Q8nhj8 homo sapien
26	385.5	29.6	598	4	Q8NHJ7	Q8nhj7 homo sapien
27	385.5	29.6	598	4	Q8NHJ2	Q8nhj2 homo sapien
28	385.5	29.6	598	4	O750I7	O750i7 homo sapien
29	383.5	29.4	650	4	O750Z4	O750z4 homo sapien
30	379.5	29.1	650	4	Q8NHJ6	Q8nhj6 homo sapien
31	379.5	29.1	651	4	Q8NHJ9	Q8nhj9 homo sapien
32	379.5	29.1	651	4	Q8NHK0	Q8nhk0 homo sapien
33	379.5	29.1	652	4	O750Z5	O750z5 homo sapien
34	379	29.0	439	4	Q8NHJ3	Q8nhj3 homo sapien
35	376	28.8	420	4	Q8NHJ7	Q8nhj7 homo sapien
36	376	28.8	420	4	Q8NHJ4	Q8nhj4 homo sapien
37	376	28.8	420	4	Q8NHJ1	Q8nhj1 homo sapien
38	376	28.8	420	4	Q8NHJ1	Q8nhj1 homo sapien
39	376	28.8	420	4	Q8NHJ4	Q8nhj4 homo sapien
40	376	28.8	420	4	Q8NHJ2	Q8nhj2 homo sapien
41	376	28.8	439	4	O15469	O15469 homo sapien
42	375	28.8	264	6	Q28109	Q28109 bos taurus
43	372.5	28.6	697	1	Q8K4V6	Q8k4v6 mus musculus
44	372.5	28.6	841	11	Q8R2Z1	Q8r2z1 mus musculus
45	371	28.5	420	4	O15470	O15470 homo sapien

ALIGNMENTS

Q9UIF2	PRELIMINARY;	PRT;	339 AA.
Q9UIF2	01-MAY-2000 (TREMBArel.13, Created)		
Q9UIF2	01-MAY-2000 (TREMBArel.13, Last sequence update)		
Q9UIF2	01-MAR-2003 (TREMBArel.23, Last annotation update)		
Q9UIF2	Platelet glycoprotein VI precursor (Platelet glycoprotein VI-1).		
Q9UIF2	GFVI.		
Q9UIF2	Homo sapiens (Human).		
Q9UIF2	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Q9UIF2	Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.		
Q9UIF2	NCBI_TaxID=9606;		
Q9UIF2	[1]		
Q9UIF2	SEQUENCE FROM N.A.		
Q9UIF2	Miyata Y.;		
Q9UIF2	"Platelet glycoprotein VI-1";		
Q9UIF2	submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.		
Q9UIF2	(2)		
Q9UIF2	SEQUENCE FROM N.A.		
Q9UIF2	PubMed=1027634;		
Q9UIF2	Ezumi Y., Uchiyama T., Takayama H.;		
Q9UIF2	"Molecular cloning, genomic structure, chromosomal localization, and		
Q9UIF2	alternative splicing forms of the platelet collagen receptor		
Q9UIF2	glycoprotein VI-1";		
Q9UIF2	Biochem. Biophys. Res. Commun. 277:27-36(2000).		
Q9UIF2	EMBL; AB035073; BAB9353.1; -		
Q9UIF2	EMBL; AB043819; BAB12245.1; -		
Q9UIF2	HSP; P43626; INKR.		
Q9UIF2	InterPro; IPR003599; IG.		
Q9UIF2	InterPro; IPR003066; IG_MHC.		
Q9UIF2	Pfam; PF00047; IG; 2.		
Q9UIF2	SMART; SM00409; IG; 2.		
Q9UIF2	Signal.		
Q9UIF2	1		
Q9UIF2	20		
Q9UIF2	POTENTIAL.		
Q9UIF2	CHAM		
Q9UIF2	21		
Q9UIF2	339		
Q9UIF2	SEQUENCE		
Q9UIF2	339 AA;		
Q9UIF2	36923 MM;		
Q9UIF2	423756595E030CC CRC64;		
Q9UIF2	100.0%;		
Q9UIF2	Score 1304;		
Q9UIF2	DB 4;		
Q9UIF2	Length 339;		

Best Local Similarity 100.0%; Pred. No. 2,3e-111;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QSGPLPKPSLOALPSSLVPLEKPYTLRCQSPGVLYLRLKSSRRYQDAVLFIPAMK 60
DB 21 QSGPLPKPSLOALPSSLVPLEKPYTLRCQSPGVLYLRLKSSRRYQDAVLFIPAMK 60
QY 61 SLAGRYRCSYQNGSLMSLPSDQLELVATGVFAKPSLSAQGPVAVSSGGVTLCCQTRYGF 120
DB 81 SLAGRYRCSYQNGSLMSLPSDQLELVATGVFAKPSLSAQGPVAVSSGGVTLCCQTRYGF 140
QY 121 DQFALYKGGDPAPKPNERNYRASFPITVTAASGTYRCVSFSRDPYLSAPSDPEL 180
DB 141 DQFALYKGGDPAPKPNERNYRASFPITVTAASGTYRCVSFSRDPYLSAPSDPEL 200
QY 181 VWTGTSVTPSRLLPTEPPSSVAEFSEATAEIVTSFTNKVFTTESRSITTSPEKSDSPAG 240
DB 201 VWTGTSVTPSRLLPTEPPSSVAEFSEATAEIVTSFTNKVFTTESRSITTSPEKSDSPAG 260
QY 241 ARQYTTKGN 249
DB 261 ARQYTTKGN 269

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RESULT 2

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ID Q9HCN6 PRELIMINARY; PRT; 620 AA.
AC Q9HCN6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Platelet glycoprotein VI-3.
GN GPI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20483673; PubMed=11027634;
RA Ezumi Y., Uchiyama T., Takayama H.;
RT "Molecular cloning, genomic structure, chromosomal localization, and
RT alternative splice forms of the platelet collagen receptor
RT glycoprotein VI".
RL Biochem. Biophys. Res. Commun. 277:27-36 (2000).
CR EMBL; AB043821; BAB:2247.1; -.
DR HSSP; P43626; INKR.
DR Genew; HGNC:4388; GP6.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003066; IG_MHC.
DR Pfam; PF00407; IG_2.
DR SMART; SMC0409; IG; 2.
SQ SEQUENCE 620 AA; 67309 MW; FEE64C5F679615 CRC64;

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Query Match 95.8%; Score 1247; DB 4; Length 620;
Best Local Similarity 100.0%; Pred. No. 8,6e-106;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QSGPLPKPSLOALPSSLVPLEKPYTLRCQSPGVLYLRLKSSRRYQDAVLFIPAMK 60
DB 21 QSGPLPKPSLOALPSSLVPLEKPYTLRCQSPGVLYLRLKSSRRYQDAVLFIPAMK 80
QY 61 SLAGRYRCSYQNGSLMSLPSDQLELVATGVFAKPSLSAQGPVAVSSGGVTLCCQTRYGF 120
DB 81 SLAGRYRCSYQNGSLMSLPSDQLELVATGVFAKPSLSAQGPVAVSSGGVTLCCQTRYGF 140
QY 121 DQFALYKGGDPAPKPNERNYRASFPITVTAASGTYRCVSFSRDPYLSAPSDPEL 180
DB 141 DQFALYKGGDPAPKPNERNYRASFPITVTAASGTYRCVSFSRDPYLSAPSDPEL 200
QY 181 VWTGTSVTPSRLLPTEPPSSVAEFSEATAEIVTSFTNKVFTTESRSITTSPEKSDSPAG 239
DB 201 VWTGTSVTPSRLLPTEPPSSVAEFSEATAEIVTSFTNKVFTTESRSITTSPEKSDSPAG 259

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RESULT 3

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ID Q9HCN7 PRELIMINARY; PRT; 321 AA.
AC Q9HCN7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Platelet glycoprotein VI-2.
GN GPI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20483673; PubMed=11027634;
RA Ezumi Y., Uchiyama T., Takayama H.;
RT "Molecular cloning, genomic structure, chromosomal localization, and
RT alternative splice forms of the platelet collagen receptor
RT glycoprotein VI".
RL Biochem. Biophys. Res. Commun. 277:27-36 (2000).
CR EMBL; AB043820; BAB:2246.1; -.
DR HSSP; P43626; INKR.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003066; IG_MHC.
DR Pfam; PF00407; IG_2.
DR SMART; SMC0409; IG; 2.
SQ SEQUENCE 321 AA; 35158 MW; 93FBF68945958345 CRC64;

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Query Match 91.6%; Score 1194; DB 4; Length 321;
Best Local Similarity 92.8%; Pred. No. 2,6e-10; Indels 18; Gaps 1;
Matches 231; Conservative 0; Mismatches 0;

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QY 1 QSGPLPKPSLOALPSSLVPLEKPYTLRCQSPGVLYLRLKSSRRYQDAVLFIPAMK 60
DB 21 QSGPLPKPSLOALPSSLVPLEKPYTLRCQSPGVLYLRLKSSRRYQDAVLFIPAMK 80
QY 61 SLAGRYRCSYQNGSLMSLPSDQLELVATGVFAKPSLSAQGPVAVSSGGVTLCCQTRYGF 120
DB 81 SLAGRYRCSYQNGSLMSLPSDQLELVATGVFAKPSLSAQGPVAVSSGGVTLCCQTRYGF 140
QY 121 DQFALYKGGDPAPKPNERNYRASFPITVTAASGTYRCVSFSRDPYLSAPSDPEL 180
DB 141 DQFALYKGGDPAPKPNERNYRASFPITVTAASGTYRCVSFSRDPYLSAPSDPEL 200
QY 181 VWTGTSVTPSRLLPTEPPSSVAEFSEATAEIVTSFTNKVFTTESRSITTSPEKSDSPAG 240
DB 201 VWTGTSVTPSRLLPTEPPSSVAEFSEATAEIVTSFTNKVFTTESRSITTSPEKSDSPAG 242
QY 241 ARQYTTKGN 249
DB 243 ARQYTTKGN 251

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RESULT 4

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ID Q8MU22 PRELIMINARY; PRT; 461 AA.
AC Q8MU22;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Leukocyte immunoglobulin-like receptor e.
GN LIRE.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxId=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21555186; PubMed=11698452;
RA Canavez F.C., Young N.T., Guehlein T.A., Rajalingam R., Khakoo S.I.,

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RA Shum B.P., Patnaik P.;
 RT "Comparison of chimpanzee and human leukocyte Ig-like receptor genes
 reveals framework and rapidly evolving genes.";
 R J. Immunol. 167:5786-5794 (2001).
 DR EMBL: AF38169; AL31878.1; -
 DR InterPro: IPR003598; IG_C2.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; IG_4.
 DR SMART: SMO0408; IGc2; 4.
 KW Immunoglobulin domain; Receptor.
 SQ SEQUENCE 481 AA; 52438 MW; 3F8C7E8724BF0FC CRC64;

Query Match 32.6%; Score 424.5; DB 6; Length 481;
 Best Local Similarity 42.3%; Pred. No. 1.7e-30;
 Matches 91; Conservative 34; Mismatches 69; Indels 21; Gaps 3;

QY 1 QSGPLPKPSLQALPSSLVPLEKPTLRCCGPGVDLYRLEKSSSRVOD-----QA 51
 DB 22 QAGPLPKPTLMAEPGVSIVMSRPVTTWCQGSLEAGYRLYKESRPRDTQVMEPRXKA 81
 QY 52 VLFIPAMKRSIAGRYCYQNGSLWSPSDQLELVATGVFAKPSLSAOPGPAVSSGCVT 111
 DB 82 RFSIPSTEDYAGRYCYRSPAGWSEFSDPLELVITGVSTPTLSALPSVYASGCVT 141
 QY 112 LQCOTRYGFDQFALYKEDPAPY-----WYRASPTITVTAHSGTYRCYS 162
 DB 142 LRCGSQKGYDHFVLMKEG--HQLPOTLDSOHLSHGSGFQALPVGVPVPSHRWFTCYG 198
 QY 163 FSSRDPYLMWAPSDPLELVITGVSTVTPSRLLPTEFP 197
 DB 199 SYANTPOVWHPDPLEILPSGVSRKPSLTLTQGP 233

RESULT 5
 Q8NHJ6 PRELIMINARY; PRT: 447 AA.
 ID Q8NHJ6
 AC Q8NHJ6;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Leukocyte immunoglobulin-like receptor-5.
 GN LIRB5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Canavez F.C.;
 RJ Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF283988; AL36992.1; -
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; IG_2.
 KW Receptor.
 SQ SEQUENCE 447 AA; 49193 MW; 6B1E83E2B107814 CRC64;

Query Match 32.1%; Score 419; DB 4; Length 447;
 Best Local Similarity 44.2%; Pred. No. 4.9e-30;
 Matches 95; Conservative 27; Mismatches 79; Indels 14; Gaps 2;

QY 1 QSGPLPKPSLQALPSSLVPLEKPTLRCCGPGVDLYRLEKSSSRVOD-----QA 51
 DB 22 QAGPLPKPTLMAEPGVSIVMSRPVTTWCQGSLEAGYRLYKESRPRDTQVMEPRXKA 81
 QY 52 VLFIPAMKRSIAGRYCYQNGSLWSPSDQLELVATGVFAKPSLSAOPGPAVSSGCVT 111
 DB 82 RFSIPSTEDYAGRYCYRSPAGWSEFSDPLELVITGVSTPTLSALPSVYASGCVT 141
 QY 112 LQCOTRYGFDQFALYKEDPAPY-----WYRASPTITVTAHSGTYRCYSFSSR 166
 DB 142 LRCGSQKGYDHFVLMKEG--HQLPOTLDSOHLSHGSGFQALPVGVPVPSHRWFTCYG 198
 QY 167 DPLYMSAPSDPLELVITGVSTVTPSRLLPTEPSSVA 201

DB 202 SHYLSHPDPLELVSGSLIEDPAPSPFRSVSTAA 236

RESULT 6
 ID Q15468 PRELIMINARY; PRT: 448 AA.
 AC Q15468;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Monocyte inhibitory receptor precursor.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Arm J.P., Nwanke C., Austen K.F.;
 RT "Molecular identification of a novel family of human immunoglobulin
 RT superfamily members that possess immunoreceptor tyrosine-based
 RT inhibitory motifs and homology to the mouse gp49b1 inhibitory
 RT receptor";
 RJ Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U91925; AB86865.1; -
 DR HSRF; P43626; INKR.
 DR GeneW; HGNC:608; LIRB4.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; IG_2.
 DR SMART: SMO0409; IG_1.
 KW Receptor; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 448
 SQ SEQUENCE 448 AA; 49297 MW; 76D1E24A82EA1399 CRC64;

Query Match 32.1%; Score 418; DB 4; Length 448;
 Best Local Similarity 44.2%; Pred. No. 6e-30;
 Matches 95; Conservative 27; Mismatches 79; Indels 14; Gaps 2;

QY 1 QSGPLPKPSLQALPSSLVPLEKPTLRCCGPGVDLYRLEKSSSRVOD-----QA 51
 DB 22 QAGPLPKPTLMAEPGVSIVMSRPVTTWCQGSLEAGYRLYKESRPRDTQVMEPRXKA 81
 QY 52 VLFIPAMKRSIAGRYCYQNGSLWSPSDQLELVATGVFAKPSLSAOPGPAVSSGCVT 111
 DB 82 RFSIPSTEDYAGRYCYRSPAGWSEFSDPLELVITGVSTPTLSALPSVYASGCVT 141
 QY 112 LQCOTRYGFDQFALYKEDPAPY-----WYRASPTITVTAHSGTYRCYFSSR 166
 DB 142 LRCGSQKGYDHFVLMKEG--HQLPOTLDSOHLSHGSGFQALPVGVPVPSHRWFTCYG 198
 QY 167 DPLYMSAPSDPLELVITGVSTVTPSRLLPTEPSSVA 201
 DB 202 SHYLSHPDPLELVSGSLIEDPAPSPFRSVSTAA 236

RESULT 7
 ID Q8NHJ5 PRELIMINARY; PRT: 448 AA.
 AC Q8NHJ5;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Leukocyte immunoglobulin-like receptor 5.
 GN LIR5.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RJ MEDLINE=20395285; PubMed=10941837;

RA Liu W.R., Kim C., Nwankwo C., Ashworth L.K., Ary J.P.;
 RT "Genomic organization of the human leukocyte immunoglobulin-like
 RT receptors within the leukocyte receptor complex on chromosome
 RT 19q13.4.";
 RL Immunogenetics 51:659-669(2000).
 DR EMBL: AF189768; AAC02024.1; -
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; IG_2.
 KW Receptor.
 SQ SEQUENCE 448 AA; 49298 MW; 9631CC446CEA1993 CRC64;
 Query Match 32.1%; Score 418; DB 4; Length 448;
 Best Local Similarity 44.2%; Pred. No. 6e-30;
 Matches 95; Conservative 27; Mismatches 79; Indels 14; Gaps 2;
 QY 1 QSGPLPKPSLQALSSIVPLEKPYTLRCQGPVGLYRLKLSRSRYOD-----CA 51
 DB 22 QAGPLPKPTLMAEGSVISMNSVTIWCQGLTARETRLDKESPAWDRQNPLEPAKKA 81
 QY 52 VLFIPAMKSLAGSYRCYQNGSLMSLPSDQLELVATGVFAKPSLAQPGPAVSSGGCVT 111
 DB 82 RFSIPKSTEDYAGRYRCYRSPVGMSPQSDPLELVMGAYSKPTLSALPPLVTSKSVT 141
 QY 112 LCQCTRYGDFQFAFYKCGDPAPY----KNPERKWRASFPITITAAHSCTYRCYSSSR 166
 DB 142 LFCGSRSPMDTFLIKERAAHPLHLRSEHQHQAEFPWSPVTSVHGCTYRCFSSHG 201
 QY 167 DPLYMSAPSDPLELVVTGTSVPSRLPTEPPSSVA 201
 DB 202 SHYLLSHPSDPLELVGSLGGRPSPTRSYSTAA 236
 RESULT 8
 Q8NU17 PRELIMINARY; PRT; 448 AA.
 AC 08NU17;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM
 DE domains), member 4.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_TaxID=9606;
 RN 11;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strauberg R.;
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC026309; AA026309.1; -
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; IG_2.
 KW Receptor.
 SQ SEQUENCE 448 AA; 49303 MW; A6155D29F7D89812 CRC64;
 Query Match 32.1%; Score 418; DB 4; Length 448;
 Best Local Similarity 44.2%; Pred. No. 6e-30;
 Matches 95; Conservative 27; Mismatches 79; Indels 14; Gaps 2;
 QY 1 QSGPLPKPSLQALSSIVPLEKPYTLRCQGPVGLYRLKLSRSRYOD-----CA 51
 DB 22 QAGPLPKPTLMAEGSVISMNSVTIWCQGLTARETRLDKESPAWDRQNPLEPAKKA 81
 QY 52 VLFIPAMKSLAGSYRCYQNGSLMSLPSDQLELVATGVFAKPSLAQPGPAVSSGGCVT 111
 DB 82 RFSIPKSTEDYAGRYRCYRSPVGMSPQSDPLELVMGAYSKPTLSALPPLVTSKSVT 141
 QY 112 LCQCTRYGDFQFAFYKCGDPAPY----KNPERKWRASFPITITAAHSCTYRCYSSSR 166
 DB 142 LFCGSRSPMDTFLIKERAAHPLHLRSEHQHQAEFPWSPVTSVHGCTYRCFSSHG 201
 QY 167 DPLYMSAPSDPLELVVTGTSVPSRLPTEPPSSVA 201

DB 202 SHYLLSHPSDPLELVGSLGGRPSPTRSYSTAA 236
 RESULT 9
 Q75021 PRELIMINARY; PRT; 448 AA.
 AC 075021;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Leukocyte immunoglobulin-like receptor-5.
 GN LIR-5.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_TaxID=9606;
 RN 11;
 RP SEQUENCE FROM N.A.
 RA Borges L., Hsu M.-L., Fanger N., Kubin M., Cosman D.;
 RJ J. Immunol. 0:0-0(1997).
 DR EMBL: AF025532; AAB87666.1; -
 DR HSSP: P43626; INKR.
 DR InterPro: IPR003589; IG.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; IG_2.
 DR SMART: SM00409; IG_1.
 SQ SEQUENCE 448 AA; 49325 MW; 76D1E0B7AD3A1399 CRC64;
 Query Match 32.1%; Score 418; DB 4; Length 448;
 Best Local Similarity 44.2%; Pred. No. 6e-30;
 Matches 95; Conservative 27; Mismatches 79; Indels 14; Gaps 2;
 QY 1 QSGPLPKPSLQALSSIVPLEKPYTLRCQGPVGLYRLKLSRSRYOD-----CA 51
 DB 22 QAGPLPKPTLMAEGSVISMNSVTIWCQGLTARETRLDKESPAWDRQNPLEPAKKA 81
 QY 52 VLFIPAMKSLAGSYRCYQNGSLMSLPSDQLELVATGVFAKPSLAQPGPAVSSGGCVT 111
 DB 82 RFSIPKSTEDYAGRYRCYRSPVGMSPQSDPLELVMGAYSKPTLSALPPLVTSKSVT 141
 QY 112 LCQCTRYGDFQFAFYKCGDPAPY----KNPERKWRASFPITITAAHSCTYRCYSSSR 166
 DB 142 LFCGSRSPMDTFLIKERAAHPLHLRSEHQHQAEFPWSPVTSVHGCTYRCFSSHG 201
 QY 167 DPLYMSAPSDPLELVVTGTSVPSRLPTEPPSSVA 201
 DB 202 SHYLLSHPSDPLELVGSLGGRPSPTRSYSTAA 236
 RESULT 10
 Q8MU23 PRELIMINARY; PRT; 631 AA.
 AC 08MU23;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Leukocyte immunoglobulin-like receptor d.
 GN LIRD.
 OS Pan troglodytes (Chimpanzee).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 CX NCBI_TaxID=9598;
 RN 11;
 RP SEQUENCE FROM N.A.
 RA MEDJ:2155186; PubMed:11698452;
 RA Caravez F.C., Young N.T., Guethlein L.A., Rajalingam R., Khakoo S.I.,
 RA Shun B.B., Parham P.;
 RT "Comparison of chimpanzee and human leukocyte Ig-like receptor genes
 RT reveals framework and rapidly evolving genes.";
 RL J. Immunol. 167:5786-5794(2001).
 DR EMBL: AF383168; AAL31877.1; -
 DR InterPro: IPR003599; IG.

DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR003006; Ig_YMC.
 DR Pfam: PF00047; Ig; 4.
 DR SMART: SM00409; Ig; 4.
 DR SMART: SM00408; IgC2; 2.
 DR PROSITE: PS00835; IG_LIKE; 2.
 KM Immunoglobulin domain; Receptor.
 SQ SEQUENCE 631 AA; 69456 MW; 10E7B706D254DEP CRC64;

Query Match 31.1%; Score 415.5; DB 6; Length 631;
 Best Local Similarity 38.1%; Pred. No. 1,6e-29;
 Matches 101; Conservative 44; Mismatches 101; Indels 19; Gaps 6;

CY 1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQGPVVDLYRLKLSSTRYCD-----CA 51
 DB 22 QAGPFPPTLMAEFGSYISWGSPTITWCGQSLLEAOBYCLYKEGSTEPMKRTNPLETRNKA 81
 QY 52 VLFIPAMKRSIAGRYRCSYONGSLWSPDQLELVATGVFAKPSLSAQGPVAVSSGGVDT 111
 DB 82 RFSIPSMTHHAGRYRCHYYSRPGMSEPSDPLELVITGVYSKPTLSALPSPVAVSSGNT 141
 QY 112 LQCTRYGDFQALYKCGD---PAPYKNPE---RWYASFPITVTAAHSGTYRCVSFS 165
 DB 142 LRCGSKGYDHFVLMKEGHEQLPRTLDSQLHSGGFQALFPVGPVTPSSSRMTFRCYVYT 201
 QY 166 RDPYLMASPSDPLELVITGVTSVTPSRLPTEPSSVAFSEATDEL--TVSFINKVFTTET 223
 DB 202 YNQGVMSPSDPLELIVTGVTSVTPSRLPTEPSSVAFSEATDEL--TVSFINKVFTTET 253
 QY 224 SRGITSITSPKESDSPAGPARQVYTKG 248
 DB 261 ERDFLPGRGQGPQ-AGLSQANFTLG 284

RESULT 11
 ID Q0M25 PRELIMINARY; PRT; 645 AA.
 AC Q0M25;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-XAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Leukocyte immunoglobulin-like receptor b.
 OS LIRB.
 SN Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
 CX NCBI_TaxID=9598;
 RN 1;
 RP SEQUENCE FROM N.A.
 RA MEDLINE=4155186; PubMed=11688452;
 RX Canavez F.C., Young N.T., Guehrlein L.A., Rajalingam R., Khakoo S.I.,
 EA Shum B.P., Parham P.;
 RT "Comparison of chimpanzee and human leukocyte Ig-like receptor genes
 RT reveals framework and rapidly evolving genes."
 RL J. Immunol. 167:5786-5794(2001).
 DR EMBL: AF383166; AAL31875.1; -
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR003006; Ig_YMC.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00409; Ig; 4.
 DR SMART: SM00408; IgC2; 3.
 DR PROSITE: PS00835; IG_LIKE; 2.
 KM Immunoglobulin domain; Receptor.
 SQ SEQUENCE 645 AA; 69898 MW; A032ED6BDEBF344 CRC64;

Query Match 31.1%; Score 408.5; DB 6; Length 645;
 Best Local Similarity 39.6%; Pred. No. 7.3e-29;
 Matches 106; Conservative 34; Mismatches 103; Indels 25; Gaps 8;
 CY 1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQGPVVD---LYRLKLSSTRYCDQAV--- 52

DB 22 QAGTLPPTLPAEDPSVITQSPPTLRCQSLSEQENHILREKKSASWIKRIQOVYKKG 81
 QY 53 -LFIAMKRSIAGRYRCSYONGSLWSPDQLELVATGVFAKPSLSAQGPVAVSSGGVDT 111
 DB 82 QPFSITWELAGRYRCHYYSRPGMSEPSDPLELVITGVYSKPTLSALPSPVAVSSGNT 141
 QY 112 LQCTRYGDFQALYKCGDPAFYKNPE-----RWYASFPITVTAAHSGTYRCYS 162
 DB 142 LQCGSLAFGFTLCKEGED---EPQCVNSQSHTLGSMWAFVSGVSPSRWVSRCYG 198
 QY 163 FSSDPLMASPSDPLELVITGVTSVTPSRLPTEPSSVAFSEATDEL--TVSFINKVFTTET 223
 DB 199 YNQMSPVMSLPSELILVPGVSKKS-LSVCGPVVAPOEILITLQCGSDVGYDRFVLY 257
 QY 221 TERSITSPKESDSPAGPARQVYTKG 248
 DB 258 KEGERDFLPGRGQGPQ-AGLSQANFTLG 284

RESULT 12
 ID O15471 PRELIMINARY; PRT; 631 AA.
 AC O15471;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Monocyte inhibitory receptor precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 CX NCBI_TaxID=9606;
 RN 1;
 RP SEQUENCE FROM N.A.
 RA Arm J.P., Nwankwo C., Austen K.F.;
 RT "Molecular identification of a novel family of human immunoglobulin
 RT superfamily members that possess immunoreceptor tyrosine-based
 RT inhibitory motifs and homology to the mouse gp49b1 inhibitory
 RT receptor";
 RT Submitted (XAR-1997) to the EMBL/GenBank/DBJ databases.
 RL EMBL: U91928; AAB68668.1; -
 DR HSBP; P43626; INKR.
 DR Genew; HGNC:6607; LIRB3.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003006; Ig_YMC.
 DR InterPro: IPR00734; Lipase.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00409; Ig; 2.
 DR PROSITE: PS00835; IG_LIKE; 1.
 DR PROSITE: PS00120; LIRASE_SER; 1.
 KM Receptor; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 631
 SQ SEQUENCE 631 AA; 69386 MW; 61CF1967B08D79FA CRC64;
 POTENTIAL INHIBITORY RECEPTOR.

Query Match 31.1%; Score 405.5; DB 4; Length 631;
 Best Local Similarity 37.0%; Pred. No. 1.3e-28;
 Matches 98; Conservative 40; Mismatches 108; Indels 19; Gaps 6;

CY 1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQGPVVDLYRLKLSSTRYCD-----CA 51
 DB 22 QAGPFPPTLMAEFGSYISWGSPTITWCGQSLLEAOBYCLYKEGSTEPMKRTNPLETRNKA 81
 QY 52 VLFIPAMKRSIAGRYRCSYONGSLWSPDQLELVATGVFAKPSLSAQGPVAVSSGGVDT 111
 DB 82 RFSIPSMTHHAGRYRCHYYSRPGMSEPSDPLELVITGVYSKPTLSALPSPVAVSSGNT 141
 QY 112 LQCTRYGDFQALYKCGD---PAPYKNPE---RWYASFPITVTAAHSGTYRCVSFS 165
 DB 142 LRCGSKGYDHFVLMKEGHEQLPRTLDSQLHSGGFQALFPVGPVTPSSSRMTFRCYVYT 201
 QY 166 RDPYLMASPSDPLELVITGVTSVTPSRLPTEPSSVAFSEATDEL--TVSFINKVFTTET 223

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Cb      202 NTPQVWHPSPDPLSLPSGVSRKPSLLTLQGP-VLADGGALLTCCGGSDVGYDFVLYKGG 260
Cy      224 SRSITTSPESSDPAAPARQVYTKG 248
Db      261 ERDPLGRPGGQPG-AGLSQANFTLG 284

RESULT 13
Q8SP05
ID      Q8SP05      PRELIMINARY;      PRT:      336 AA.
AC      Q8SP05;
DT      01-JUN-2002 (Tremblrel: 21, Created)
DT      01-JUN-2002 (Tremblrel: 21, Last sequence update)
DT      01-OCT-2002 (Tremblrel: 22, Last annotation update)
DE      NK receptor KIR2DL1.
GN      KIR2DL1.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      1.
RP      SEQUENCE FROM N.A.
RX      MEDLINE=2185885; Pubmed=11870625;
RA      McQueen K.L., Wilhelm B.T., Harden K.C., Wager D.L.;
RT      "Evolution of NK receptors: a single Ly49 and multiple KIR genes in
RT      the cow."
RL      Eur. J. Immunol. 32:810-817(2002).
DR      EMBL: AY075103; ALN82801.1;
DR      InterPro: IPR003599; IG_
DR      InterPro: IPR003066; IG_MHC.
DR      Pfam: PF00347; IG_2.
DR      SMART: SMC0409; IG_2.
DR      SMART: SMC0409; IG_2.
KM      Receptor.
SQ      SEQUENCE 336 AA: 36667 MW: 8484645AF089D02 CRC64;

Query Match      30.8%; Score 401; DB 6; Length 336;
Best Local Similarity 45.1%; Pred. No. 1,5e-28;
Matches 96; Conservative 24; Mismatches 79; Indels 14; Gaps 5;

Cy      1 QSGPLPKPSLALPSSLVPLEKPYTLRCQGPVGVYRLEKLSRRYQD-DAVLF----- 54
Db      22 QEGGHDKPFLSNWSPVVPFGSCHVTILFCQSPFLGFRRLHKDRINVPBLGILFNKEL 81
Cy      55 IPAWKSLAGRYRC-SYCN-GSLWLSPLDQLSVATGVFAKPSLSAQGPVAVSGGVY 111
Db      82 MGPLYTAHAGTYRCHGHYSHLPNLSAPSDPLEVVTGLSKKPSLSAQGPVAVRSGENV 141
Cy      112 LCCOTRYGFGFOFALYKGG-----DPAYKYPKPKYRASPTITVTAAHSTYRCYFSGR 166
Db      142 LVCSSESAPFQFHLRREGVNLGRPLAGRGPRCALQXEFPLGFGTPDHSVYRCYGSFTR 202
Cy      167 DFYLSAPSDPLELVVTGTVTPSRLLPTEPPSS 199
Db      202 SPYKWSDSDPYLAISTGNSSSSGPHTKNSN 234

RESULT 14
Q75022
ID      Q75022      PRELIMINARY;      PRT:      631 AA.
AC      Q75022;
DT      01-NOV-1998 (Tremblrel: 08, Created)
DT      01-NOV-1998 (Tremblrel: 08, Last sequence update)
DT      01-MAR-2003 (Tremblrel: 23, Last annotation update)
DE      Leukocyte immunoglobulin-like receptor-3.
GN      LIR-3.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      11.
RP      SEQUENCE FROM N.A.

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RA      Borges L., Heu M.-L., Fanger N., Kubin M., Cosman C.;
RL      J. Immunol. 0:0-0(1997).
DR      EMBL: AF025533; AAB87667.1;
DR      HSSP: P43626; INKR.
DR      InterPro: IPR003599; IG_
DR      InterPro: IPR007110; IG-like.
DR      InterPro: IPR003066; IG_MHC.
DR      InterPro: IPR000734; LIPase.
DR      Pfam: PF00047; IG_3.
DR      SMART: SMC0409; IG_1.
DR      PROSITE: PS00835; IG_LIKE; 1.
DR      PROSITE: PS00120; LIPASE_SRR; 1.
SQ      SEQUENCE 631 AA: 69226 MW: 87718042F9C25 CRC64;

Query Match      30.7%; Score 400.5; DB 4; Length 631;
Best Local Similarity 25.0%; Pred. No. 3,8e-28;
Matches 117; Conservative 43; Mismatches 81; Indels 227; Gaps 9;

Cy      1 QSGPLPKPSLALPSSLVPLEKPYTLRCQGPVGVYRLEKLSRRYQD-----QA 52
Db      22 QAGPPKPTLWAFQSVISWGSPTIWCQGLSAQEVQDKEGPEPLDRNKPPEPKYA 81
Cy      52 VLFIPAMKSLAGRYRCGYONCSLWS;PSDQLSVATGVFAKPSLSAQGPVAVSGGVY 111
Db      82 RPSLPSYTCQHHAGRYRCHYSSAGWSESDPLELVVTGAYSKPLSLAPSVVAGGNT 141
Cy      112 LCCOTRY----- 118
Db      142 LRCSQKRYHGFVLMKEGEHQLPRTLDSCQLHSGGFQALPFVGVVNSHMFYCYIYM 202
Cy      119 -----GFQDFLLYKGD 130
Db      202 NTPRWHPSPDPLSLPSGVSRKPSJTLQGPVLAFGQSJTLCCGSDVGYDFVLYKGE 262
Cy      131 ----PARYKPE-----RW----- 140
Db      262 RDLFDRPGQPCAGLSQANFTLGPVFSNGQRYRCYAHNLSSKWSAPSDPLNLMACI 321
Cy      141 -----YASAF 145
Db      322 YDTVLSAQGPPTVASGENVTLLCSMWQPFLLTREGAHPPLRSMYGAHKYQAEF 381
Cy      146 PIITVTAHSTGYCYSSSSRDPLYMSAPSDPLELVVTGTVTPSRLLPTEPPSS--VAEF 203
Db      382 FMSPTSAHAGTYRCHYSSNPYLHSPSSPLELVVSGHGGSLPPTGPTPGJGRY 441
Cy      204 SEATYELTVSFTNKVF-----TETSRSITTSPESSD--SPAGPA 241
Db      442 LEVLIGVAVFVLLFLVLLFLLLRQRHRSKRTSDQKRTDGRAGAA 489

RESULT 15
Q8MJ27
ID      Q8MJ27      PRELIMINARY;      PRT:      643 AA.
AC      Q8MJ27;
DT      01-OCT-2002 (Tremblrel: 22, Created)
DT      01-OCT-2002 (Tremblrel: 22, Last sequence update)
DT      01-MAR-2003 (Tremblrel: 23, Last annotation update)
DE      Leukocyte immunoglobulin-like receptor 8.
GN      LIR8.
OS      Pan troglodytes (Chimpanzee).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX      NCBI_TaxID=9598;
RN      11.
RP      SEQUENCE FROM N.A.
RX      MEDLINE=2155186; Pubmed=11698452;
RA      Canavez F.C., Young N.T., Guehlein L.A., Rajalingam R., Krakoo S.;
RT      Comparison of chimpanzee and human leukocyte Ig-like receptor genes
RT      reveals framework and rapidly evolving genes."
RL      J. Immunol. 167:5786-5794(2001).
DR      EMBL: AF383164; AAL31873.1;

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DR InterPro; IPR003593; Ig.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003066; Ig_MHC.
DR Pfam; PF08047; Ig; 3.
DR SMART; SMC0409; IG; 4.
DR SMART; SMC0408; IGC2; 2.
DR Immunoglobulin domain; Receptor.
SC SEQUENCE 643 Aa; 70504 XM; BECC8F940B5F55AC CRC64

Query Match	30.7%	Score 430	DB 6	Length 643
Best Local Similarity	44.2%	Pred. NO. 4.4e-28		
Matches 91	Conservative 27	Mismatches 74	Indels 14	Gaps 2

Oy	QSGPLPSPSLQALPSSSLVPLEKPVTLRCGGPGVGVLYLEKISSRRQDQAVLFIPMKR	60
Db	22 QAGTLPRPTLMAFSPASVIRGKPEVILWCGPLETEYEYRLDYGLEFMANERKNPLEPGAKA	91
Oy	61 SL-----AGRYRCSYONGSLWLSPSDQLELVATVFAKPSLSAOPGAVSGSGCVT	111
Db	82 KFHLSLVYVMSAQRNYCYETPRAGMSEPDPLELVATGYFAEPTLLALPSVYASGGNV	141
Oy	112 LQCGTRYGQDFALVYECDDPAP-----YKNPERKWRASFPITITVTAHSGTGYCSFSR	166
Db	142 LQCGTRGGLTLFVLVEEOKLPRILYSQKLPGKPSRALPFGVPTPSFRMRFRCYYYPRK	201
Oy	167 DFTYMSAPDPLVLVVTGTSVTPSRLL	192
Db	202 NPQVMSHPSCLELIVFGVSRKPSLL	227

Search completed: November 10, 2003, 06:15:00
Job time : 37 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 10, 2003, 06:15:04 ; Search time 21 Seconds

(Without alignments)
1140.286 Million cell updates/sec

Title: US-09-503-387-9

Perfect score: 1304

Sequence: 1 QSGPLPKXSLQALPSLVPL.....SPKSDSPAGPAKYTKGN 249

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616682 residues

Total number of hits satisfying chosen parameters: 283309

Minimum DB seq length: 0
Maximum DB seq length: 202000000

Post-processing: Minimum Match 3%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1304	100.0	339	2	glycoprotein Vi-1
2	381	29.2	466	2	Killer cell inhibi
3	375	28.6	264	2	FC gamma 2 recepto
4	372.5	28.6	841	2	Killer cell inhibi
5	365.5	28.0	635	2	Killer cell inhibi
6	345.5	26.5	680	2	Killer cell inhibi
7	320.5	24.6	444	2	KIR (C1-11) NK rec
8	314.5	24.1	296	2	cell surface glyco
9	314	24.1	348	2	natural killer cel
10	312.5	24.0	341	2	natural killer ass
11	312.5	24.0	444	2	KIR (C1-2) NK rec
12	305	23.4	239	2	cell surface glyco
13	302	23.4	335	2	cell surface glyco
14	299	22.9	287	2	cell surface glyco
15	295.5	22.7	427	2	KIR (C1-5) NK rec
16	291.5	22.4	455	2	Killer cell inhibi
17	280	21.5	303	2	KIR (C1-5) NK rec
18	275.5	21.1	1327	2	membrane glycopro
19	145	11.1	237	2	immunoglobulin-1k
20	142.5	10.9	474	1	alpha-1-B-glycopro
21	141.5	10.9	184	2	hypothetical prote
22	126.5	9.7	3707	2	heparan sulfate pr
23	124.5	9.5	267	2	Fc-gamma RIIR-ai
24	118.5	9.1	267	2	Fc-gamma (IGG) rec
25	115	8.8	283	1	FC gamma (IGG) rec
26	114.5	8.8	1259	2	Bravo/Nr-CAM cell
27	113.5	8.7	1268	1	neural cell adhe
28	111.5	8.6	4391	1	perlecan precursor
29	1.0	8.4	270	2	Fc-gamma receptor

30	109.5	8.4	4162	2	Connectiv...itin -
31	107	8.2	261	2	Fc gamma (IGG) rec
32	106	8.1	285	2	Fc gamma (IGG) rec
33	105.5	8.1	330	2	Fc gamma (IGG) rec
34	105.5	8.1	330	2	Fc gamma (IGG) rec
35	104.5	8.0	267	2	Fc gamma (IGG) rec
36	103.5	7.9	1612	2	Fc gamma receptor
37	101	7.7	388	2	ductal protein - mo
38	101	7.7	3375	2	hypothetical prote
39	100	7.7	257	2	hypothetical prote
40	100	7.7	336	2	IGS Fc receptor a1
41	100	7.7	1367	1	Fc gamma (IGG) rec
42	99	7.6	739	2	glucan 1,4-alpha-g
43	98.5	7.6	1651	2	vascular cell adhe
44	98.5	7.6	3149	2	transmembrane rece
45	98	7.5	1256	2	BP1F1 protein - hu
					CD0 protein - rat

ALIGNMENTS

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RESULT 1
JC7509
Glycoprotein Vi-1 - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: JC7509; PC7101
R:Rezum, Y.; Uchiyama, T.; Takayama, H.
Biochem. Biophys. Res. Commun. 277, 27-36, 2000
A:Title: Molecular cloning, genomic structure, chromosomal localization, and alterna
A:Reference number: JC7509; MUCD:20489673; PMID:11027654
A:Contents: Platelet
A:Accession: JC7509
A:Molecule type: mRNA
A:Residues: 1-339 <EZY>
A:Cross-references: DDBJ:AB043819
A:Accession: PC7101
A:Molecule type: protein
A:Residues: 28-4162-79;114-142 <EZY>
C:Comment: This protein, which belongs to the immunoglobulin superfamily, is the major
or gamma chain as a signal transducing subunit, and plays some roles in cancer cells
C:Genetics:
A:Gene: GPVI-1
A:Map position: 19q13.4
A:Intons: 62/1; 95/1; 353/1; 638/1; 692/1; 752/1; 803/1
C:Keywords: glycoprotein; immunoglobulin; platelet

Query Match
100.0%; Score 1304; DB 2; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.8e-95;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 QSGPLPKXSLQALPSLVPLRKQSGPGVDLYRLEKSSSRVQCAVLFIPMKR 60
|||||
21 QSGPLPKXSLQALPSLVPLRKQSGPGVDLYRLEKSSSRVQCAVLFIPMKR 80
|||||

61 SLARRKSYONGSLWLSLPSDQLVATGVFAKSLDAQPGPAVSSGGVTLVQCTRYGF 120
|||||
81 SLARRKSYONGSLWLSLPSDQLVATGVFAKSLDAQPGPAVSSGGVTLVQCTRYGF 140
|||||

121 DQFLYKSGDPAFKNRERWRASFTITVTAASGTIRCYSPSSRPFLMSASDPELE 180
|||||
141 DQFLYKSGDPAFKNRERWRASFTITVTAASGTIRCYSPSSRPFLMSASDPELE 200
|||||

181 VVTGTSVTPSRPLPPEPSSVAEFAELTVSSTNKVFTTETSRSTTSPKSDSPAGP 240
|||||
201 VVTGTSVTPSRPLPPEPSSVAEFAELTVSSTNKVFTTETSRSTTSPKSDSPAGP 260
|||||

241 ARQYTKGN 249
|||||
261 ARQYTKGN 269
|||||

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RESULT 2

JC5897

killer cell inhibitory receptor p91 precursor - human

C.Species: Homo sapiens (map)

C.Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 05-Nov-1999

C.Accession: JC5897

R.Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.; Chay

J. Biochem. 123, 358-368, 1998

A.Title: Genomic structures and chromosomal location of p91, a novel murine regulatory

A.Reference number: JC5894; MUID:99218758; PMID:9538215

A.Accession: JC5897

A.Status: nucleic acid sequence not shown

A.Molecule type: mRNA

A.Residues: 1-466 <YAM>

A.Cross-references: GB:AF041034; NID:92791689; PCD:AA96928.1; PID:92791693

C.Comment: This protein function as inhibitory cell-surface molecule against cell active

C.Genetics:

A.Map position: 19q13.3-13.4

F.1-23/Domain: signal sequence #status predicted <SIG>

Query Match

Best local similarity 29.2%; Score 381; DB 2; Length 466;

Matches 102; Conservative 37; Mismatches 104; Indels 24; Gaps 5;

1 QSGPLPKPSLQALPSSLVPLEKPYTLRQGFPGVD---LYLEKLS--SRYPD---QAV 52

22 CAGHLPKPTLWAEFGSVILQSPVTLRQGSGLQAEVHLVRENKASWVRICQPKNQ 81

53 LFPAMKSLAGRCYCSYQNGSLMSLPDQLELVATGVFAKPS-SAGCPAYSSGGCVT 112

82 FPLSTWENHAGRHCCQYSHNSSEVSDPLELVATGVFAKPSVTLGGVNT 141

113 QCGTRYGDFQALYKEDPAPYKPERM-----YRASPIITVTAHSGTYRCYSF 163

142 QCVGVAFDGFILCKEGED---EHQRLNLSHSHRAGSSRAIFSGVFPSPRKRSHRCYCY 198

164 SSRDPYLMASPSDPLELVATGVFAKPS-SAGCPAYSSGGCVT 221

199 DLSNPYVMSSPSCLELIVPGVSKKPS-LSYQGPVYAFESLTLQCVSDVGDVFLYK 257

222 ETSRSTTSPKESDPSAGPARYTKG 248

258 EGERDRLQLPGRFQF-AQSSANFTLG 283

RESULT 3

146220

FC Gamma 2 receptor precursor - bovine

C.Species: Bos primigenius taurus (cattle)

C.Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999

C.Accession: 146020; S53115

Rizhang, G.; Young, U.R.; Tregaskes, C.A.; Sopp, P.; Howard, C.J.

J. Immunol. 155, 1534-1541, 1995

A.Title: Identification of a novel class of mammalian FC gamma receptor.

A.Reference number: 146020; MUID:95363119; PMID:7636215

A.Accession: 146020

A.Status: preliminary; translated from GB/EX3L/DDBU

A.Molecule type: mRNA

A.Residues: 1-264 <ZEA>

A.Cross-references: EXBL:Z37506; NID:9732571; PID:CA85736.1; PID:9732572

C.Keywords: immunoglobulin receptor

Query Match

Best local similarity 28.8%; Score 375; DB 2; Length 264;

Matches 85; Conservative 23; Mismatches 68; Indels 23; Gaps 4;

1 QSGPLPKPSLQALPSSLVPLEKPYTLRQGFPGVD---LYLEKLS--SRYPD---QAV 51

22 CAGTTPKPIIMAEPSVPLGSSVTLQCGPNTKSFELNKEGSTPMNHPLESPDKA 81

52 VIFPAMKSLAGRCYCSYQNGSLMSLPDQLELVATGVFAKPS-SAGCPAYSSGGCVT 105

82 NFPISTWENHAGRHCCQYSHNSSEVSDPLELVATGVFAKPSVTLGGVNT 141

113 QCGTRYGDFQALYKEDPAPYKPERM-----YRASPIITVTAHSGTYRCYSF 163

142 QCVGVAFDGFILCKEGED---EHQRLNLSHSHRAGSSRAIFSGVFPSPRKRSHRCYCY 198

164 SSRDPYLMASPSDPLELVATGVFAKPS-SAGCPAYSSGGCVT 221

199 DLSNPYVMSSPSCLELIVPGVSKKPS-LSYQGPVYAFESLTLQCVSDVGDVFLYK 257

222 ETSRSTTSPKESDPSAGPARYTKG 248

258 EGERDRLQLPGRFQF-AQSSANFTLG 283

RESULT 4

146220

FC Gamma 2 receptor precursor - bovine

C.Species: Bos primigenius taurus (cattle)

C.Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999

C.Accession: 146020; S53115

Rizhang, G.; Young, U.R.; Tregaskes, C.A.; Sopp, P.; Howard, C.J.

J. Immunol. 155, 1534-1541, 1995

A.Title: Identification of a novel class of mammalian FC gamma receptor.

A.Reference number: 146020; MUID:95363119; PMID:7636215

A.Accession: 146020

A.Status: preliminary; translated from GB/EX3L/DDBU

A.Molecule type: mRNA

A.Residues: 1-264 <ZEA>

A.Cross-references: EXBL:Z37506; NID:9732571; PID:CA85736.1; PID:9732572

C.Keywords: immunoglobulin receptor

Query Match

Best local similarity 28.8%; Score 375; DB 2; Length 264;

Matches 85; Conservative 23; Mismatches 68; Indels 23; Gaps 4;

1 QSGPLPKPSLQALPSSLVPLEKPYTLRQGFPGVD---LYLEKLS--SRYPD---QAV 51

22 CAGTTPKPIIMAEPSVPLGSSVTLQCGPNTKSFELNKEGSTPMNHPLESPDKA 81

52 VIFPAMKSLAGRCYCSYQNGSLMSLPDQLELVATGVFAKPS-SAGCPAYSSGGCVT 105

82 NFPISTWENHAGRHCCQYSHNSSEVSDPLELVATGVFAKPSVTLGGVNT 141

113 QCGTRYGDFQALYKEDPAPYKPERM-----YRASPIITVTAHSGTYRCYSF 163

142 QCVGVAFDGFILCKEGED---EHQRLNLSHSHRAGSSRAIFSGVFPSPRKRSHRCYCY 198

164 SSRDPYLMASPSDPLELVATGVFAKPS-SAGCPAYSSGGCVT 221

199 DLSNPYVMSSPSCLELIVPGVSKKPS-LSYQGPVYAFESLTLQCVSDVGDVFLYK 257

222 ETSRSTTSPKESDPSAGPARYTKG 248

258 EGERDRLQLPGRFQF-AQSSANFTLG 283

RESULT 5

146220

FC Gamma 2 receptor precursor - bovine

C.Species: Bos primigenius taurus (cattle)

C.Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999

C.Accession: 146020; S53115

Rizhang, G.; Young, U.R.; Tregaskes, C.A.; Sopp, P.; Howard, C.J.

J. Immunol. 155, 1534-1541, 1995

A.Title: Identification of a novel class of mammalian FC gamma receptor.

A.Reference number: 146020; MUID:95363119; PMID:7636215

A.Accession: 146020

A.Status: preliminary; translated from GB/EX3L/DDBU

A.Molecule type: mRNA

A.Residues: 1-264 <ZEA>

A.Cross-references: EXBL:Z37506; NID:9732571; PID:CA85736.1; PID:9732572

C.Keywords: immunoglobulin receptor

Query Match

Best local similarity 28.8%; Score 375; DB 2; Length 264;

Matches 85; Conservative 23; Mismatches 68; Indels 23; Gaps 4;

1 QSGPLPKPSLQALPSSLVPLEKPYTLRQGFPGVD---LYLEKLS--SRYPD---QAV 51

22 CAGTTPKPIIMAEPSVPLGSSVTLQCGPNTKSFELNKEGSTPMNHPLESPDKA 81

52 VIFPAMKSLAGRCYCSYQNGSLMSLPDQLELVATGVFAKPS-SAGCPAYSSGGCVT 105

82 NFPISTWENHAGRHCCQYSHNSSEVSDPLELVATGVFAKPSVTLGGVNT 141

113 QCGTRYGDFQALYKEDPAPYKPERM-----YRASPIITVTAHSGTYRCYSF 163

142 QCVGVAFDGFILCKEGED---EHQRLNLSHSHRAGSSRAIFSGVFPSPRKRSHRCYCY 198

164 SSRDPYLMASPSDPLELVATGVFAKPS-SAGCPAYSSGGCVT 221

199 DLSNPYVMSSPSCLELIVPGVSKKPS-LSYQGPVYAFESLTLQCVSDVGDVFLYK 257

222 ETSRSTTSPKESDPSAGPARYTKG 248

258 EGERDRLQLPGRFQF-AQSSANFTLG 283

106 SGGDVLQCGTRYGDFQALYKEDPAPYKPERM-----YRASPIITVTAHSGTYRC 160

142 PGENTLQCGTRYGDFQALYKEDPAPYKPERM-----YRASPIITVTAHSGTYRC 201

161 YFSRSSDPYLMASPSDPLELV 182

202 YRSLSYRPLSLQSPSLALIV 223

RESULT 4

killer cell inhibitory receptor p91A precursor - mouse

C.Species: Mus musculus (house mouse)

C.Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 17-Mar-1999

C.Accession: JC5894

R.Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.;

J. Biochem. 123, 358-368, 1998

A.Title: Genomic structures and chromosomal location of p91, a novel murine regula

A.Reference number: JC5894; MUID:98218758; PMID:9538215

A.Accession: JC5894

A.Status: nucleic acid sequence not shown

A.Molecule type: DNA

A.Residues: 1-841 <YAM>

A.Cross-references: GB:AF040946

C.Comment: This protein function as inhibitory cell-surface molecule against cell ac

C.Genetics:

A.Map position: 7

F.1-23/Domain: signal sequence #status predicted <SIG>

F.24-841/Product: killer cell inhibitory receptor p91A #status predicted <MAT>

F.25-118, 119-220, 221-315, 316-418, 419-517, 518-618/Domain: extracellular Ig-like #stat

F.636-675/Domain: cytoplasmic #status predicted <CTM>

F.676-765/Domain: cytoplasmic #status predicted <CTT>

Query Match

Best local similarity 28.6%; Score 372.5; DB 2; Length 841;

Matches 80; Conservative 35; Mismatches 76; Indels 17; Gaps 3;

2 SGPPLPKPSLQALPSSLVPLEKPYTLRQGFPGVD---LYLEKLS--SRYPD---QAV 53

220 SGNLQKPTIKAEPSVPLGSSVTLQCGPNTKSFELNKEGSTPMNHPLESPDKA 279

54 -FIPAMKSLAGRCYCSYQNGSLMSLPDQLELVATGVFAKPS-SAGCPAYSSGGCVT 110

280 FPISTWENHAGRHCCQYSHNSSEVSDPLELVATGVFAKPSVTLGGVNT 141

113 QCGTRYGDFQALYKEDPAPYKPERM-----YRASPIITVTAHSGTYRCYSF 164

142 QCVGVAFDGFILCKEGED---EHQRLNLSHSHRAGSSRAIFSGVFPSPRKRSHRCYCY 198

164 SSRDPYLMASPSDPLELVATGVFAKPS-SAGCPAYSSGGCVT 221

199 DLSNPYVMSSPSCLELIVPGVSKKPS-LSYQGPVYAFESLTLQCVSDVGDVFLYK 257

222 ETSRSTTSPKESDPSAGPARYTKG 248

258 EGERDRLQLPGRFQF-AQSSANFTLG 283

RESULT 5

146220

FC Gamma 2 receptor precursor - bovine

C.Species: Bos primigenius taurus (cattle)

C.Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999

C.Accession: 146020; S53115

Rizhang, G.; Young, U.R.; Tregaskes, C.A.; Sopp, P.; Howard, C.J.

J. Immunol. 155, 1534-1541, 1995

A.Title: Identification of a novel class of mammalian FC gamma receptor.

A.Reference number: 146020; MUID:95363119; PMID:7636215

A.Accession: 146020

A.Status: preliminary; translated from GB/EX3L/DDBU

A.Molecule type: mRNA

A.Residues: 1-635 <YAM>

A.Cross-references: GB:AF041036; NID:92791693; PID:AA96928.1; PID:92791694

C.Comment: This protein function as inhibitory cell-surface molecule against cell ac

F.1-23/Domain: signal sequence #status predicted <SIG>

F.24-118, 119-220, 221-315, 316-418, 419-517, 518-618/Domain: extracellular Ig-like #statu

Query Match

Best local similarity 28.6%; Score 372.5; DB 2; Length 841;

Matches 80; Conservative 35; Mismatches 76; Indels 17; Gaps 3;

2 SGPPLPKPSLQALPSSLVPLEKPYTLRQGFPGVD---LYLEKLS--SRYPD---QAV 53

220 SGNLQKPTIKAEPSVPLGSSVTLQCGPNTKSFELNKEGSTPMNHPLESPDKA 279

54 -FIPAMKSLAGRCYCSYQNGSLMSLPDQLELVATGVFAKPS-SAGCPAYSSGGCVT 110

280 FPISTWENHAGRHCCQYSHNSSEVSDPLELVATGVFAKPSVTLGGVNT 141

113 QCGTRYGDFQALYKEDPAPYKPERM-----YRASPIITVTAHSGTYRCYSF 164

142 QCVGVAFDGFILCKEGED---EHQRLNLSHSHRAGSSRAIFSGVFPSPRKRSHRCYCY 198

164 SSRDPYLMASPSDPLELVATGVFAKPS-SAGCPAYSSGGCVT 221

199 DLSNPYVMSSPSCLELIVPGVSKKPS-LSYQGPVYAFESLTLQCVSDVGDVFLYK 257

222 ETSRSTTSPKESDPSAGPARYTKG 248

258 EGERDRLQLPGRFQF-AQSSANFTLG 283

Query Match 28.0%; Score 365.5; DB 2; Length 635;
 Best Local Similarity 37.5%; Pred. No. 4,4e-21;
 Matches 78; Conservative 38; Mismatches 75; Indels 17; Gaps 3;

QY 2 SGPFLPKPSLOALPSSVPLEKPYTLRCQGPFGVDYLRLEKSSSRVQDAV-----53
 DB 220 SCHLQKPTIKAFEGSVIASKRAMTIWCGNLDAEVFLINMSQKQSTQCTLOQPNKGR 279
 QY 54 -FPAKRSIAGRYRCYQNGSLMSLPDQLELVATGVFA--KPSLSAOPGPAVSSGGDV 110
 DB 280 FFPSVYTOHAGQYRCYCYSAGMSQPSDLELVATGVIEHYKPRLSV-PSPVYIAGGM 339
 QY 111 TLCCQTRRGFDQFALYKEDG-----PAPYKNERKYSFPIITVTAHSGTYRCYSF 164
 DB 340 LHCACSDPHYDKTLTKEDKKFGNSLDTEHISSRQYALFTIGFTPHHTGFRYCYGF 399
 QY 165 SRDPYLSAPSDPLELVATGVTSVTPSR 192
 DB 400 KNAFQLMSVSPDLQGITLISGLSKKPSLL 427

RESULT 6
 C35895
 Killer cell inhibitory receptor p913 precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 05-Nov-1999
 C:Accession: J03895
 R:Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Chya, J.; Biochem. 123, 358-368, 1998
 A:Title: Genomic structures and chromosomal location of p91, a novel murine regulatory T
 A:Reference number: J03894; MIM:198218758; PMID:9539215
 A:Accession: J03895
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-680 <YAN>
 A:Cross-references: GB:A041935; NID:92791691; P:CN:AA096927.1; PID:92791692
 C:Comment: This protein function as inhibitory cell-surface molecule against cell activa
 C:Genetics:
 A:Map position: 7
 F:1-23/Domain: signal sequence #status predicted <Sig>
 F:24-118,119-220,221-315,316-418,419-517,518-618/Domain: extracellular Ig-like hstratus p
 F:619-674/Domain: transmembrane #status predicted <TM>
 F:675-680/Domain: cytoplasmic #status predicted <CYT>

Query Match 26.5%; Score 345.5; DB 2; Length 680;
 Best Local Similarity 36.1%; Pred. No. 1.8e-19;
 Matches 75; Conservative 39; Mismatches 77; Indels 17; Gaps 3;

QY 2 SGPFLPKPSLOALPSSVPLEKPYTLRCQGPFGVDYLRLEKSSSRVQDAV-----53
 DB 220 SCHLQKPTIKAFEGSVIASKRAMTIWCGNLDAEVFLINMSQKQSTQCTLOQPNKGR 279
 QY 54 -FPAKRSIAGRYRCYQNGSLMSLPDQLELVATGVFA--KPSLSAOPGPAVSSGGDV 110
 DB 280 FFPSVYTOHAGQYRCYCYSAGMSQPSDLELVATGVIEHYKPRLSV-PSPVYIAGGM 339
 QY 111 TLCCQTRRGFDQFALYKEDG-----PAPYKNERKYSFPIITVTAHSGTYRCYSF 164
 DB 340 LHCACSDPHYDKTLTKEDKKFGNSLDTEHISSRQYALFTIGFTPHHTGFRYCYGF 399
 QY 165 SRDPYLSAPSDPLELVATGVTSVTPSR 192
 DB 400 KNAFQLMSVSPDLQGITLISGLSKKPSLL 427

RESULT 7
 G01925
 KIR (cl-11) NK receptor precursor protein - human
 C:Species: Homo sapiens (man)
 C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
 A:Accession: G01925; T61726
 R:Kagmann, N.
 submitted to the EMBL Data Library, June 1995

A:Reference number: G08782
 A:Accession: G01925
 A:Status: preliminary; translated from GB/EXBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-444 <NAG>
 A:Cross-references: EMBL:U30274; NID:G1004360; P:CN:AA052522.1; PID:G1004361
 R:Colonna, V.; Samaridis, J.
 Science 268, 405-408, 1995
 A:Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA
 A:Reference number: A56247; X01D:95232526; PMID:7716543
 A:Accession: L61726
 A:Status: preliminary; translated from GB/EXBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-444 <RES>
 A:Cross-references: GB:L41269; NID:9780307; P:CN:AA069970.1; PID:9780308
 C:Genetics:
 A:Gene: NKAT-3
 A:Map position: 19

Query Match 24.6%; Score 320.5; DB 2; Length 444;
 Best Local Similarity 38.6%; Pred. No. 9.9e-18;
 Matches 83; Conservative 22; Mismatches 81; Indels 29; Gaps 5;

QY 7 KPSLOALPSSVPLEKPYTLRCQGPFGVDYLRLEKSSSRVQDAV-----LFI 55
 DB 123 KPSLHAPGFLVSGERVILQMSDIMEHFLEKIGSDPRLVCGINDVSKAFST 182
 QY 56 PAKRSIAGRYRC-----SYQNGSLMSLPDQLELVATGVFAKPSLSAOPGPAVSSGG 108
 DB 183 GPMALAGRYRCGVTHTPYQ---LSAPSDPLELVATGVPEKPSLSAOPGPAVSSGG 238
 QY 109 DVTLCCQTRRGFDQFALYKEDGPAKYKP-----ERKYSFPIITVTAHSGTYRCYSF 163
 DB 239 SVTSCSSRSRYVHYHSRFGAHERLPAVKRKNRFQADFLL--GPAHGGYRCYCFGS 295
 QY 164 SRDPYLSAPSDPLELVATGVTSVTPSR 198
 DB 297 FRHSPYEMSPSDPLELVATGVTSVTPSR 331

RESULT 8
 B51434
 Cell surface glycoprotein gp49b form 2 precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 05-Nov-1999
 C:Accession: B51434
 R:Castells, M.C.; Wu, X.; Alm, J.P.; Austen, K.F.; Kacz, H.R.
 J. Biol. Chem. 269, 8393-8401, 1994
 A:Title: Cloning of the gp49b gene of the immunoglobulin superfamily and demonstra
 A:Reference number: A51434; MIM:94179223; PMID:8112564
 A:Accession: B51434
 A:Status: preliminary
 A:Molecule type: DNA; mRNA
 A:Residues: 1-296 <CAS>
 A:Cross-references: GB:U05265; NID:9475446; P:CN:AAA17799.1; PID:9475448; GB:U05266;
 C:Genetics:
 A:Gene: GP49B
 A:Introns: 12/3; 24/2; 119/2; 220/1; 232/1; 249/3; 272/1
 C:Keywords: alternative splicing; glycoprotein

Query Match 24.1%; Score 314.5; DB 2; Length 296;
 Best Local Similarity 35.5%; Pred. No. 1.8e-17;
 Matches 81; Conservative 33; Mismatches 93; Indels 21; Gaps 5;

QY 1 QSGPLPKPSLOALPSSVPLEKPYTLRCQGPFGVDYLRLEKSSSRVQDAV-----CA 51
 DB 22 QAGHLKPTIWAEGSVIAVTSVITWCGSMEAGYHLVKEKSVNPMEDQVPETRKKA 81
 QY 52 VLFIPAKRSIAGRYRCYQNGSLMSLPDQLELVATGVFAKPSLSAOPGPAVSSGGDV 111
 DB 82 KFNIPSMYTSYAGIKCYEAGAFSHSDMELVMGAYNPPLSYTPSSNVTSSYGIS 141
 QY 112 LCCQTRRGFDQFALYKEDG-----DPAPYKNERKYSFPIITVTAHSGTYRCYSF 163

Db 142 FSCSSIVFRFLIQGKGLSWLDSQHQAQPSY-AIFVLAIVPMHNGTFRQCYV 199
 QY 164 SSRDPYMSASDPLVLTGTSVTPSRLECEPPSSVAEF-SEATAEI 210
 Db 200 FRNRPQWMSKPSNGLDMISPTK-DQSTETEDDASVKNCSNNNEJ 246

RESULT 9

A56247

Natural killer cell-associated protein - human

C:Species: Homo sapiens (man)

C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 35-Nov-1999

C/Accession: A56247

R:Colonna, M.; Santaridis, J.

A:Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B

A:Reference number: A56247; MIMD:95232526; PMID:7716543

A:Accession: A56247

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-348 <RDS>

A:Cross-references: GB:U4167; NID:G780303; PIDN:AAA6986.1; PID:G780304

C:Genetics:

A:Gene: GDS.NKAT1

A:Cross-references: GDB:698165

A:Map position: 19

Query Match

Best Local Similarity 32.3%; Pred. No. 2, 4e-17;

Matches 93; Conservative 36; Mismatches 105; Indels 54; Gaps 10;

QY 7 KPSTQALPSSLVPLEKPYTRCCGPPGVLDYRLKLSSSRYQD-----QAVL 53
 Db 28 KPSTLAHPGLVKSSEFVILQCMWDVFEHFLHR--EGVFNLTLLIGEHHDGVSKANF 85
 QY 54 FIPAKRSIAGRYRC-----SYQNGSLWSPDQLELVATGVFAKPSLSAQGPVAVSS 106
 Db 86 SIGPMODLAGTYRCYSGVTHSPYQ---VSAPSDPLDIVITGLYKPSLSAQGPVLA 141
 QY 107 GGVTLQCCRTYGFDPALYKESDPAVYKNP-----FRWYFASFPILITVAHSGTYRCY 161
 Db 142 GENVTLSCSSRSYDWHLSRBEBAHERLPAQPKXNCTQADFPL--GPAHGGTYRCF 199
 QY 162 SFSSRDPLYMSAPDPLVLTGTSVTPSRLECEPPSSVA-----EPSEATAEIYTSF-- 214
 Db 200 GSPHDSPEYMSKSDPLVLTGTSVTPSRLECEPPSSVA-----EPSEATAEIYTSF-- 259
 QY 215 -----TNK-----VFTETSRSTSPKESDPAVYKNP-----EPSEATAEIYTSF-- 249
 Db 260 LFFLLRWCSNKKMAVMDQESAKNTANSEDSDE-QDPQVITTYQLN 306

RESULT 10

161725

Natural killer associated transcript 2 - human

C:Species: Homo sapiens (man)

C>Date: 23-May-1998 #sequence_revision 23-May-1998 #text_change 05-Nov-1999

C/Accession: 161725

R:Colonna, M.; Santaridis, J.

A:Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B

A:Reference number: A56247; MIMD:95232526; PMID:7716543

A:Accession: 161725

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-341 <RDS>

A:Cross-references: GB:U41268; NID:G780305; PIDN:AAA6986.1; PID:G780306

C:Genetics:

A:Gene: NKAT-2

Query Match

Best Local Similarity 37.4%; Pred. No. 3, 1e-17;

Matches 82; Conservative 24; Mismatches 76; Indels 37; Gaps 7;

QY 7 KPSTQALPSSLVPLEKPYTRCCGPPGVLDYRLKLSSSRYQD-----QAVL 53
 Db 28 KPSTLAHPGLVKSSEFVILQCMWDVFEHFLHR--EGVFNLTLLIGEHHDGVSKANF 85
 QY 54 FIPAKRSIAGRYRC-----SYQNGSLWSPDQLELVATGVFAKPSLSAQGPVAVSS 106
 Db 86 SIGPMODLAGTYRCYSGVTHSPYQ---VSAPSDPLDIVITGLYKPSLSAQGPVLA 141
 QY 107 GGVTLQCCRTYGFDPALYKESDPAVYKNP-----FRWYFASFPILITVAHSGTYRCY 161
 Db 142 GENVTLSCSSRSYDWHLSRBEBAHERLPAQPKXNCTQADFPL--GPAHGGTYRCF 199
 QY 162 SFSSRDPLYMSAPDPLVLTGTSVTPSRLECEPPSSVA-----EPSEATAEIYTSF-- 214
 Db 200 GSPHDSPEYMSKSDPLVLTGTSVTPSRLECEPPSSVA-----EPSEATAEIYTSF-- 259
 QY 215 -----TNK-----VFTETSRSTSPKESDPAVYKNP-----EPSEATAEIYTSF-- 249
 Db 260 LFFLLRWCSNKKMAVMDQESAKNTANSEDSDE-QDPQVITTYQLN 306

RESULT 11

G01924

KIR (G1-2) NK receptor precursor - human

N.A.terrate names: Killer cell inhibitory receptor

C:Species: Homo sapiens (man)

C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999

C/Accession: G01924; G01945

R:Wagtmann, N.

A:Reference number: G08780

A:Accession: G01924

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-444 <WAG>

A:Cross-references: EMBL:U030273; NID:G1004358; PIDN:AA52521.1; PID:G1004359

R:U. Andread, A.; Chang, C.; Franz-Bacon, K.; McClanahan, T.; Phillips, J.H.; Tanter, I.

submitted to the EMBL Data Library, July 1995

A:Reference number: G08908

A:Accession: G01945

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-444 <DNA>

A:Cross-references: EMBL:U01416; NID:G973405; PIDN:AA023725.1; PID:G973406

C:Genetics:

A:Gene: NKBL

Query Match

Best Local Similarity 38.1%; Pred. No. 4, 2e-17;

Matches 82; Conservative 22; Mismatches 82; Indels 29; Gaps 5;

QY 7 KPSTQALPSSLVPLEKPYTRCCGPPGVLDYRLKLSSSRYQDQAV-----QAVL 53
 Db 123 KPSTLAHPGLVKSSEFVILQCMWDVFEHFLHR--EGVFNLTLLIGEHHDGVSKANF 85
 QY 56 PAMKRSIAGRYRC-----SYQNGSLWSPDQLELVATGVFAKPSLSAQGPVAVSSG 108
 Db 183 GPMVLAALAGTYRCYSGVTHSPYQ---VSAPSDPLDIVITGLYKPSLSAQGPVLA 141
 QY 109 GGVTLQCCRTYGFDPALYKESDPAVYKNP-----FRWYFASFPILITVAHSGTYRCY 161
 Db 239 SVTLSCSSRSYDWHLSRBEBAHERLPAQPKXNCTQADFPL--GPAHGGTYRCF 199
 QY 164 SSRDPYMSASDPLVLTGTSVTPSRLECEPPSSVA-----EPSEATAEIYTSF-- 214
 Db 297 FRHSPYMSKSDPLVLTGTSVTPSRLECEPPSSVA-----EPSEATAEIYTSF-- 259

RESULT 12

G02630

FcalphaRb - human

C:Species: Homo sapiens (man)

C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998

C/Accession: G02630

R:van Dijk, T.B.; Morton, H.C.; Caldenhoven, E.; Bracke, M.; Raaijmakers, J.A.M.; Lan

submitted to the EMBL Data Library, April 1996

A:Reference number: H01508

A:Accession: G02630

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-239 <VAN>

A:Cross-references: EMBL:U56236; NID:g1326228; PDB:g1326229

Query Match

Best Local Similarity 23.4%; Score 305; DB 2; Length 239;
Best Local Similarity 36.7%; Pred. No. 7.7e-17;

Matches 72; Conservative 34; Mismatches 78; Indels 12; Gaps 2;

QY 1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQSPGVLYLEKLSRSSRYD-----CA 5;

DB 22 QAGHLPRPIIWAEGSVTLAVTSITWCQGSKEAGYHLYKESVNPMDTQVLELRNKA 8;

QY 52 VLFIPAMKRLAGRYCSYONGSJMPLSPDQLELVATGVFAKSLASAGPFAVSSGDT 111

DB 82 KENIPSMITTSYAGIYKCYESAAGFSEHSDAEVLVYGAENPSLSLYSSNVTSGVSI 141

QY 112 LCQOTRYGFDQFALYKREG-----CPAPYKNPERKVRASPIITVTAAHSGTYRCS 163

DB 142 FSCSSSVIFGRFLLIQGKGLSWTLDSCHQANQPSV--ATVLDVAVTPNHNCTFRCYGY 199

QY 164 SSDDPYLWASPSPLLELVVTGTVTSRSLPTEPPSSVAEPSEATAEIYVSF 214

DB 200 FRNEPQWKSRSKNSLDMISETK-DQSSPTPE--DGLFTQKILIGLVUSF 247

RESULT 14

JH0332

IGA (Fc) receptor, myeloid cell (CD89) precursor - human

N:Alternate names: myeloid glycoprotein CD89

C:Species: Homo sapiens (man)

C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-Nov-1999

C:Accession: JH0332; 137224; S14405

R:Kaliszewski, C.R.; March, C.J.; Schoenborn, M.A.; Gimpel, S.; Shen, L.

J. Exp. Med. 172, 1665-1672, 1990

A:Title: Expression cloning of a human Fc receptor for Iga.

A:Reference number: JH0332; MUID:91079769; PMID:2258698

A:Accession: JH0332

A:Molecule type: mRNA

A:Residues: 1-287 <MAL>

A:Cross-references: GB:X54150; NID:g131329; PDB:1A8089.1; PDB:g131330

A:Experimental source: myeloid cell liver V937

Ride W.C., P.; Norton, H.C.; Capel, P.J.; van de Winkel, J.G.

J. Immunol. 155, 1203-1209, 1995

A:Title: Structure of the gene for the human myeloid Iga Fc receptor (CD89).

A:Reference number: 137224; MUID:95363085; PMID:7636188

A:Accession: 137224

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-287 <RES>

A:Cross-references: EMBL:X87767; NID:g963641; PDB:1A61039.1; PDB:g1054737

A:Gene: GDB:FCAR; CD89

A:Cross-references: GDB:127543; OMIM:147045

A:Map position: 19q13.2-19q13.4

A:Introns: 12/1; 24/1; 121/1; 217/1

C:Keywords: glycoprotein; immunoglobulin receptor; transmembrane protein

F.1-21/Domain: signal sequence status predicted <SIG>

F.22-287/Product: Iga receptor Fc alpha #status predicted <MFC>

F.228-246/Domain: transmembrane #status predicted <TRA>

F.65,79,141,177,186/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 22.9%; Score 299; DB 2; Length 287;

Best Local Similarity 36.4%; Pred. No. 2.9e-16;

Matches 71; Conservative 34; Mismatches 78; Indels 12; Gaps 2;

QY 1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQSPGVLYLEKLSRSSRYD-----CA 49

DB 22 QEGDFPMFPIIAKSSPVILPDGSVKIQQAIREAVLTQJMTIKSTYREIGRLKFWNET 81

QY 50 QAVLFIPAMKRLAGRYCSYONGSJMPLSPDQLELVATGVFAKSLASAGPFAVSSGDT 109

DB 82 DPEFVIDHMANAKARQCCYRIGHYRFRYSDTLELVYTLGXGRFLSADSGVLMPEGN 141

QY 110 VTLQOTRY-GFDQFALYKREGDPAPYKNPERKVRASPIITVTAAHSGTYRCSFSSSDP 166

DB 142 ISLTCSAHIPFDRFSLAKEGLSLPDQSGGHPANFSLGPVDLNVSGIYRCYGMWRSP 201

QY 169 YLMSAPSDPCELVVTG 184

DB 202 YLMSFSPNALLEVVTG 217

RESULT 15

G02034

Killer cell inhibitory receptor - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999

C:Accession: G02034

R.D'Andrea, A.; Chang, C.; Faurz-Racon, K.; McCleanahan, T.; Phillips, J.H.; Lanier,

submitted to the EMBL Data Library, August 1995

A:Reference number: G09086

A:Accession: G02034

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-427 <DXA>

A:Cross-references: EMBL:U33328; NID:g995756; PDB:1AAC3726.1; PDB:g995757

A:Gene: NKB1B

Query Match

Best Local Similarity 22.7%; Score 295.5; DB 2; Length 427;

Matches 38.3%; Pred. No. 8.8e-16;

Matches 77; Conservative 21; Mismatches 74; Indels 29; Gaps 5;

QY KPSLQAIPSSVLAEKPYLVKCCGPGCVLVLYEKLSSSRVQDAV-----LF 55
Db KPSLALFPGCLVSGSERVILQCSMDIMEHFFLHKEGSKDPSELVQIHDGYSKANFST 182
QY 56 PAMKRLAGRYRC-----SYONGSLWLSPSDQLELVATGVFAKPSLQAQPGHVASG 109
Db 193 GPYMLALAGTYRCYGSVTHTPYQ---LSAPSDPLDIVTGYEKPSPLSNQPGKXOAGS 235
QY 109 DVTLCQCTRYGFGQFALYKEGSDAPYKDP---ERWYRASFPILITVTAHSGTYRYSF 163
Db 239 SVTLSCSSRSSTYNYHLSSREGANHEFLPFAVRKVRKRTQADPFLP-GPATHCGRYCFGS 296
QY 164 SSRDPYLMSAPSDPELVLTG 184
Db 297 FRHSRYEWSQSDPLLVSTG 317

Search completed: November 10, 2003, 06:20:37
Job time : 23 secs